

Delaval, Jan

8/652

From: Gambel, Phillip
Sent: Wednesday, December 04, 2002 12:59 PM
To: Delaval, Jan
Cc: Chan, Christina
Subject: 09/754004

jan

please perform a sequence and a sequence interference search for

ussn 09 / 754004

SEQ ID NO: 1

SEQ ID NO: 2

thanx

phillip gambel
art unit 1644
308-3997

Room 8B03

1644 mailbox 9e12

or i can pick up when ready. thanx

christina

please okay rush

sorry, i thought i had sequence search done already on this one

thanx

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
CM1 1E07 - 703-308-4498
jan.delaval@uspto.gov

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
 Art Unit: _____ Phone Number 30 _____ Serial Number: _____
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If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

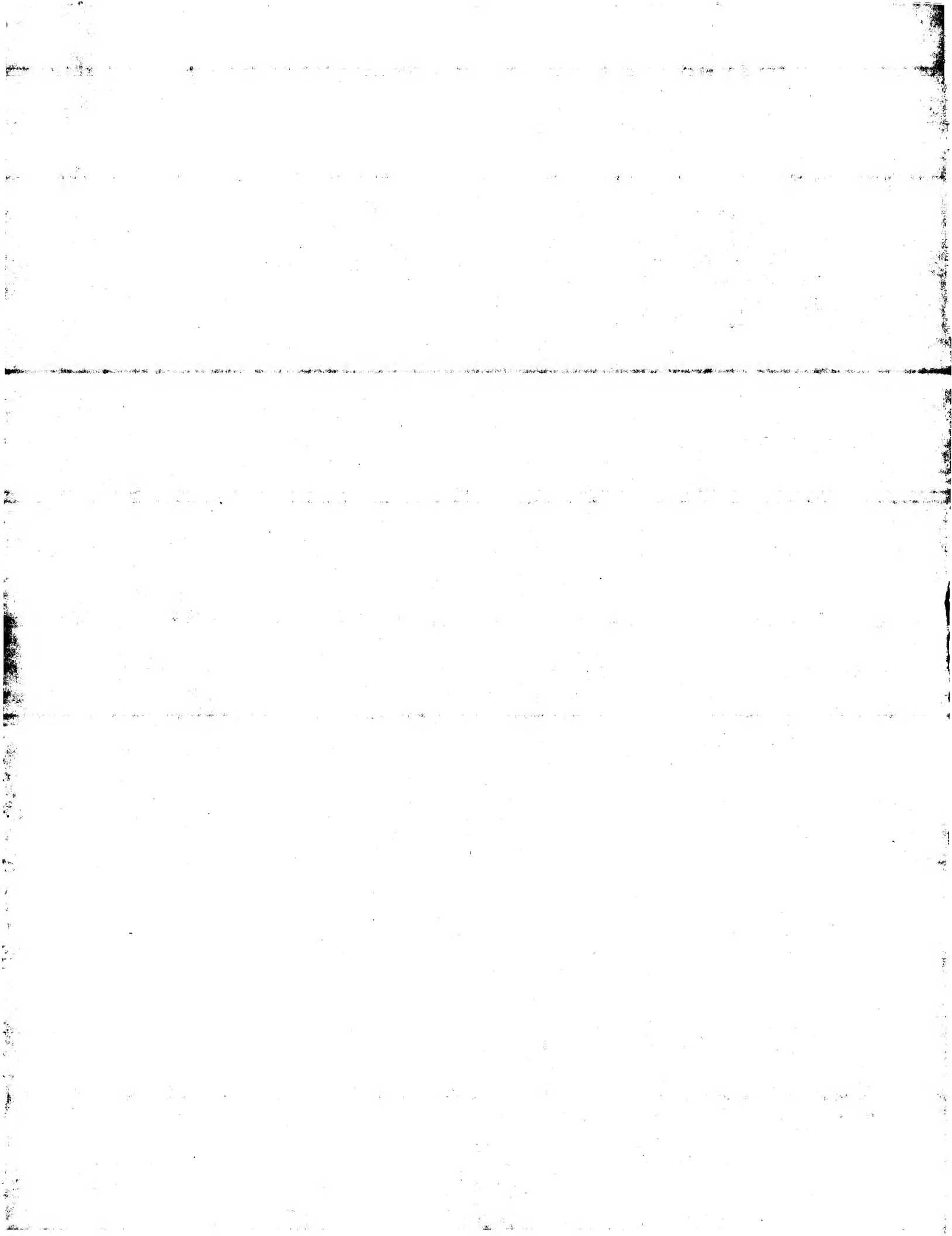
Earliest Priority Filing Date: _____

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
CM1 1E07 - 703-308-4498
jan.delaval@uspto.gov

STAFF USE ONLY

Searcher: NA Sequence (#) STN
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 Online Time: + 15 Other Other (specify)



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 4, 2002, 13:21:33 : Search time 11.3684 Seconds

(without alignments)
135.300 Million cell updates/sec

Title: US-09-754-004-1

Sequence: 1 YSOVLFKGGCGPSTHV 16

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	89	100.0	233	1 QMHUN	tumor necrosis fac
2	89	100.0	233	1 S22052	tumor necrosis fac
3	89	100.0	234	1 JQ1344	tumor necrosis fac
4	83	93.3	233	1 S11688	tumor necrosis fac
5	79	88.8	232	1 S12606	tumor necrosis fac
6	74	83.1	185	2 S52715	tumor necrosis fac
7	74	83.1	233	1 S24642	tumor necrosis fac
8	69	77.5	193	2 S06192	tumor necrosis fac
9	69	77.5	234	1 JH0529	tumor necrosis fac
10	69	77.5	235	1 QMNSN	tumor necrosis fac
11	69	77.5	235	2 JU0029	tumor necrosis fac
12	65	73.0	235	2 T54490	tumor necrosis fac
13	59	66.3	234	1 A25451	tumor necrosis fac
14	50	56.2	197	1 JH0309	tumor necrosis fac
15	50	56.2	204	1 S17289	tumor necrosis fac
16	49	55.1	204	1 S24641	tumor necrosis fac
17	45.5	51.1	278	2 A49266	fas ligand - bov
18	45.5	51.1	281	2 T38707	fas ligand - rat
19	45	50.6	360	2 D56617	fas ligand - precu
20	44.5	50.0	279	2 A53062	fas ligand - mouse
21	44	49.4	202	1 B27303	tumor necrosis fac
22	44	49.4	202	1 JN0869	tumor necrosis fac
23	44	49.4	491	2 E97159	general secretion
24	43	48.3	104	1 CCPS5A	cytochrome c551 pr
25	41.5	46.6	319	2 AE0036	probable ATP/GTP-b
26	40.5	45.5	262	2 E75478	conserved hypotnet
27	40	44.9	132	2 S45097	1k transport prot
28	40	44.9	162	2 H83073	hypothetical prote
29	40	44.9	454	2 JC7123	caspsase-9 long cha

30	40	44.9	611	2 F70325	conserved hypotnet
31	40	44.9	752	2 T50450	hypothetical prote
32	39	43.8	132	2 S45100	42k transport prot
33	39	43.8	227	2 D83521	probable pili asse
34	39	43.8	251	2 S74482	UDP-N-acetyl-D-man
35	39	43.8	308	2 B72203	hypothetical prote
36	39	43.8	416	2 S75321	serine/threonine-s
37	39	43.8	621	2 T22904	hypothetical prote
38	39	43.8	1266	1 B7C1AB	bontoxilysin (EC 3
39	38.5	43.3	266	2 AE0979	probable transcrip
40	38.5	43.3	282	2 S47795	hypothetical prote
41	38.5	43.3	318	2 A90797	hypothetical prote
42	38.5	43.3	318	2 D85657	hypothetical prote
43	38.5	43.3	407	2 B47757	retrovirus-related
44	38.5	43.3	607	2 A47757	retrovirus-related
45	38	42.7	123	2 D70182	hypothetical prote

ALIGNMENTS

RESULT 1

tumor necrosis factor alpha precursor [validated] - human

N:Alternate names: cachectin; TNFA

C:Species: Homo sapiens (man)

C>Date: 28-Aug-1985 #sequence-revision 28-Aug-1985 #text-change 08-Dec-2000

C:Accession: A93585; S36153; A93551; A44189; B61478; I5311; S62610; I54522; A01646;

R:Nedwin, G.E.; Naylor, S.L.; Sakaguchi, A.Y.; Smith, D.; Jarrett-Nedwin, J.; Pennica

Nucleic Acids Res. 13, 6361-6373, 1985

A:Title: Human lymphotoxin and tumor necrosis factor genes: structure, homology and c

A:Reference number: A93585; MUID:86016093; PMID:2955927

A:Accession: A93585

A:Molecule type: DNA

A:Residues: 1-233 <NED>

A:Cross-references: GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210

R:Rits, F.J.M.; Bougueleret, L.; Prieur, S.; Caterina, D.; Primas, G.; Perrot, V.; Ju

Nature Genet. 3, 137-145, 1993

A:Title: Dense Alu clustering and a potential new member of the NFkapab family with

A:Reference number: S36152; MUID:93272029; PMID:849947

A:Accession: S36153

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-233 <IRI>

A:Cross-references: EMBL:Z15026; NID:g37211; PIDN:CA478745.1; PID:g37212

R:Pennica, D.; Nedwin, G.E.; Hayflick, J.S.; Seeburg, P.H.; Derynck, R.; Palladino, M

Nature 312, 724-729, 1984

A:Title: Human tumour necrosis factor: precursor structure, expression and homology t

A:Reference number: A93551; MUID:85086244; PMID:6392892

A:Accession: A93551

A:Molecule type: mRNA

A:Residues: 1-233 <PEN>

A:Cross-references: GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210

A>Note: The nucleotide sequence was submitted to the EMBL Data Library, August 1992

R:Mang, A.M.; Cressy, A.A.; Ladner, M.B.; Lin, L.S.; Strickler, J.; Van Arsdel, J.N

Science 228, 149-154, 1985

A:Title: Molecular cloning of the complementary DNA for human tumor necrosis factor.

A:Reference number: A44189; MUID:85142190; PMID:3856324

A:Accession: A44189

A:Molecule type: mRNA

A:Residues: 1-62, 'S', '64-233 <MAN>

A:Cross-references: GB:M10968; NID:g339737; PIDN:AAA61198.1; PID:g339738

R:Fukuda, S.; Ando, S.; Sanou, O.; Tanai, M.; Fujii, M.; Masaki, N.; Nakamura, K.I.;

Lymphokine Res. 7, 175-185, 1988

A:Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta

A:Reference number: A61478; MUID:88301617; PMID:2841543

A:Accession: B61478

A:Molecule type: protein

A:Residues: 83-102;109-119;121-128, 'X', '130-131;142-144, 'X', '146, 'XXX', '150-152;159-174;

R:Marmenout, A.; Franssen, L.; Tavernier, J.; Van Der Heyden, J.; Tilard, R.; Kawashim

Eur. J. Biochem. 152, 515-522, 1985

A:Title: Molecular cloning and expression of human tumor necrosis factor and comparis

A:Reference number: I53311; MUID:86030296; PMID:3932069
 A:Accession: I53311
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-233 <MAR>
 A:Cross-references: GB:M26331; NID:g3339763; PIDN:AAA36758.1; PID:g3339764
 A:Experimental source: U-937 cells
 R:Takakura-Yamamoto, R.; Yamamoto, S.; Fukuda, S.; Kurimoto, M.
 Eur. J. Biochem. 235, 431-437, 1996
 A:Title: O-Glycosylated species of natural human tumor-necrosis factor-alpha.
 A:Reference number: S62610; MUID:96202967; PMID:8631363
 A:Accession: S62610
 A:Molecule type: protein
 A:Residues: 77-99 <TAK>
 R:Alfonso, S.; Richiardi, P.M.
 Immunogenetics 39, 150-154, 1994
 A:Title: A polymorphic variation in a putative regulation box of the TNFA promoter region
 A:Reference number: I54522; MUID:94102809; PMID:7903959
 A:Accession: I54522
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-8 <DAL>
 A:Cross-references: GB:S68530; NID:9544751
 R:Stevenson, F.T.; Bursten, S.L.; Locksley, R.M.; Lovett, D.H.
 J. Exp. Med. 176, 1053-1062, 1992
 A:Title: Myristyl acylation of the tumor necrosis factor alpha precursor on specific lys
 A:Reference number: A59163; MUID:93018820; PMID:1402651
 R:Aggarwal, B.B.; Kohr, W.J.; Haas, P.E.; Moffat, B.; Spencer, S.A.; Henzel, W.J.; Brink
 J. Biol. Chem. 260, 2345-2354, 1985
 A:Title: Human tumor necrosis factor. Production, purification, and characterization.
 A:Reference number: A92511; MUID:85130974; PMID:3871770
 A:Contents: annotation; disulfide bond
 C:Comment: Secreted from mitogen-activated macrophages within 4-24 hours after induction
 out detriment to normal cells. It can also act synergistically with interferon gamma to
 C:Comment: TNF-alpha and -beta (lymphokine) are the products of different genes closely
 ut are produced by different cell types and have different induction kinetics.
 C:Genetics:
 A:Gene: GDB:TNF; TNFA
 A:Cross-references: GDB:120441; OMIM:191160
 A:Map position: 6p21.3-6p21.3
 A:Introns: 62/3; 78/1; 94/1
 C:Complex: homotrimer
 C:Superfamily: tumor necrosis factor
 C:Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lipoprotein; lymphokine; mac
 F:1-76/Domain: propeptide #status predicted <PRO>
 F:77-233/Product: tumor necrosis factor #status experimental <MAT>
 F:19,20/Binding site: myristate (Lys) (covalent) #status experimental
 F:81/Binding site: carbohydrate (Ser) (covalent) (partial) #status experimental
 F:145-177/Disulfide bonds: #status experimental

Query Match 100.0%; Score 89; DB 1; Length 233;
 Best Local Similarity 100.0%; Pred. No. 2.3e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YSQVLFKGGGCPSTHV 16
 |||
 Db 135 YSQVLFKGGGCPSTHV 150

RESULT 2
 S22052
 Tumor necrosis factor alpha precursor - baboon
 C:Species: Papio sp. (baboon)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
 C:Accession: S22052
 R:Sanjanwala, M.; Edwards, A.
 submitted to the EMBL Data Library, September 1991
 A:Description: Baboon Tumor Necrosis Factor Derived from Sequences of Genomic DNA.
 A:Reference number: S22052
 A:Accession: S22052
 A:Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-233 <SAN>
 A:Cross-references: EMBL:X62141; NID:g338159; PIDN:CAA44068.1; PID:g338160
 C:Genetics:
 A:Introns: 62/3; 78/1; 94/1
 C:Superfamily: tumor necrosis factor
 C:Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein
 F:19,20/Binding site: myristate (Lys) (covalent) #status predicted
 F:81/Binding site: carbohydrate (Ser) (covalent) #status predicted
 F:145-177/Disulfide bonds: #status predicted

Query Match 100.0%; Score 89; DB 1; Length 233;
 Best Local Similarity 100.0%; Pred. No. 2.3e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YSQVLFKGGGCPSTHV 16
 |||
 Db 135 YSQVLFKGGGCPSTHV 150

RESULT 3
 J01344
 tumor necrosis factor alpha precursor - horse
 N:Alternate names: cachectin; TNF alpha
 C:Species: Equus caballus (domestic horse)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
 C:Accession: J01344
 R:Su, X.; Morris, D.D.; McGraw, R.A.
 Gene 107, 319-321, 1991
 A:Title: Cloning and characterization of gene TNF alpha encoding equine tumor necrosi
 A:Reference number: J01344; MUID:92084125; PMID:1748301
 A:Accession: J01344
 A:Molecule type: DNA
 A:Residues: 1-234 <SUH>
 A:Cross-references: GB:M64087; NID:g164244; PIDN:AAA30959.1; PID:g164245
 C:Comment: This protein is an important proximal mediator of endotoxemia.
 C:Genetics:
 A:Gene: TNF-alpha
 A:Introns: 62/3; 79/1; 95/1
 C:Superfamily: tumor necrosis factor
 C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; m
 F:78-234/Product: tumor necrosis factor alpha #status predicted <TNM>
 F:19,20/Binding site: myristate (Lys) (covalent) #status predicted
 F:82/Binding site: carbohydrate (Ser) (covalent) #status predicted
 F:146-178/Disulfide bonds: #status predicted

Query Match 100.0%; Score 89; DB 1; Length 234;
 Best Local Similarity 100.0%; Pred. No. 2.4e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YSQVLFKGGGCPSTHV 16
 |||
 Db 136 YSQVLFKGGGCPSTHV 151

RESULT 4
 S11688
 tumor necrosis factor alpha precursor - cat
 C:Species: Felis silvestris catus (domestic cat)
 C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 04-Feb-2000
 C:Accession: S11688
 R:McGraw, R.A.; Coffee, B.W.; Otto, C.M.; Drews, R.T.; Rawlings, C.A.
 Nucleic Acids Res. 18, 5563, 1990
 A:Title: Gene sequence of feline tumor necrosis factor alpha.
 A:Reference number: S11688; MUID:91016660; PMID:2216740
 A:Accession: S11688
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-233 <MCG>
 A:Cross-references: EMBL:X54000; NID:g1084; PIDN:CAA37948.1; PID:g295777
 C:Genetics:
 A:Introns: 62/3; 78/1; 94/1
 C:Superfamily: tumor necrosis factor
 C:Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein

F:19/20/Binding site: myristate (lys) (covalent) #status predicted
F:81/Binding site: carbohydrate (Ser) (covalent) #status predicted
F:145-177/Disulfide bonds: #status predicted

Query Match 93.3%; Score 83; DB 2; Length 233;
Best Local Similarity 93.8%; Pred. No. 2,4e-06;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YSOVLFKGGCPCSTHV 16
||||| |||||||
Db 135 YSOVLFKGGCPCSTHV 150

RESULT 5

S12606
tumor necrosis factor alpha precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C:Accession: S12606; S17290; S18965; I46659

R:Drews, R.T.; Coffee, B.W.; Prestwood, A.K.; McGraw, R.A.
Nucleic Acids Res. 18, 5564, 1990

A:Title: Gene sequence of porcine tumor necrosis factor alpha.
A:Reference number: S12606; MUID:91016861; PMID:2216741

A:Accession: S12606
A:Molecule type: DNA
A:Residues: 1-232 <DBE>

A:Cross-references: EMBL:X54001; NID:g2135; PIDN:CAA37949.1; PID:g2136
R:Kuhnert, P.; Weichrich, C.; Peterhans, E.; Pauli, U.
Gene 102, 171-178, 1991

A:Title: The porcine tumor necrosis factor-encoding genes: sequence and comparative anal
A:Reference number: S17289; MUID:91340150; PMID:1874444
A:Accession: S17290

A:Molecule type: DNA
A:Residues: 1-232 <KUH>

A:Cross-references: EMBL:X54859; NID:g2132; PIDN:CAA36639.1; PID:g2134
A:Note: the authors translated the codon GAG for residue 202 as Gly

R:Choi, C.S.; Mollitor, T.W.; Lin, G.F.; Murrugh, M.P.
submitted to the EMBL Data Library, January 1991

A:Description: Complete nucleotide sequence of a cDNA encoding porcine tumor necrosis fa
A:Reference number: S18965

A:Accession: S18965
A:Molecule type: mRNA
A:Residues: 1-232 <CHO>

A:Cross-references: EMBL:X57321; NID:g2137; PIDN:CAA40591.1; PID:g2138
R:Pauli, U.; Beutler, B.; Peterhans, E.
Gene 81, 185-191, 1989

A:Title: Porcine tumor necrosis factor alpha: Cloning with the polymerase chain reaction
A:Reference number: I46659; MUID:90034181; PMID:2478420
A:Accession: I46659

A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 44-232 <PAU>

A:Cross-references: GB:M29079; NID:g164694; PIDN:AAA31128.1; PID:g164695
C:Genetics:
A:Introns: 62/3; 78/1; 93/1

C:Superfamily: tumor necrosis factor
C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; myri
F:1-77/Domain: propeptide #status predicted <PRO>
F:78-232/Product: tumor necrosis factor alpha #status predicted <MAT>
F:19/20/Binding site: myristate (lys) (covalent) #status predicted
F:81/Binding site: carbohydrate (Ser) (covalent) #status predicted
F:144-176/Disulfide bonds: #status predicted

Query Match 88.8%; Score 79; DB 1; Length 232;
Best Local Similarity 87.5%; Pred. No. 1.1e-05;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 YSOVLFKGGCPCSTHV 16
|||||:|||||:|
Db 134 YSOVLFKGGCPCSTHV 149

RESULT 6

S52715
tumor necrosis factor alpha precursor - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)
C:Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 04-Feb-2000
C:Accession: S52715

R:Mertens, B.; Gaidulis, L.
submitted to the EMBL Data Library, March 1995

A:Description: Cloning and sequence analysis of cDNAs encoding bovine CD40 ligand and
A:Reference number: S52715

A:Accession: S52715
A:Molecule type: mRNA
A:Residues: 1-185 <MER>

A:Cross-references: EMBL:Z48808; NID:g755701; PIDN:CAA88743.1; PID:g755702
C:Superfamily: tumor necrosis factor
C:Keywords: glycoprotein
F:33/Binding site: carbohydrate (Ser) (covalent) #status predicted
F:97-129/Disulfide bonds: #status predicted

Query Match 83.1%; Score 74; DB 2; Length 185;
Best Local Similarity 92.9%; Pred. No. 6.2e-05;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YSOVLFKGGCPCST 14
|||||:|||||
Db 87 YSOVLFKGGCPCST 100

RESULT 7

S24642
tumor necrosis factor alpha precursor - bovine

C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C:Accession: I46047; S24642

R:Clude, I.; Cleuter, Y.; Keltmann, R.; Burry, A.; Droogmans, L.
Cytokine 5, 336-341, 1993

A:Title: Cloning and characterization of the tandemly arranged bovine lymphotoxin and
A:Reference number: I46046; MUID:94083525; PMID:8260599

A:Accession: I46047
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-233 <CL2>

A:Cross-references: EMBL:Z14137; NID:g796; PIDN:CAA78511.1; PID:g798
C:Genetics:
A:Gene: TNFA

A:Introns: 62/3; 78/1; 94/1
C:Superfamily: tumor necrosis factor
C:Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein

F:20/Binding site: myristate (lys) (covalent) #status predicted
F:81/Binding site: carbohydrate (Ser) (covalent) #status predicted
F:145-177/Disulfide bonds: #status predicted

Query Match 83.1%; Score 74; DB 1; Length 233;
Best Local Similarity 92.9%; Pred. No. 7.6e-05;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YSOVLFKGGCPCST 14
|||||:|||||
Db 135 YSOVLFKGGCPCST 148

RESULT 8

S06192
tumor necrosis factor alpha precursor - goat (fragment)

N:Alternate names: cachectin; TNF alpha
C:Species: Capra aegagrus hircus (domestic goat)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 31-Jan-2000
C:Accession: S06192; S41867

R:Goldstein, I.M.; Henner, D.; Talhouk, A.
submitted to the EMBL Data Library, March 1989

A:Reference number: S06192
A:Accession: S06192
A:Molecule type: mRNA

```

A:Residues: 1-193 <GOL>
A:Cross-references: EMBL:X14828; NID:g9992; PIDN:CAA32937.1; PID:g993
R:Rimstad, E.
submitted to the EMBL Data Library, January 1994
A:Reference number: S41867
A:Accession: S41867
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 36-36, 'S', 40-78, 'A', 80-88, 'N', 90-114, 'O', 116-123, 'D', 125-144, 'G', 145-173, 'L'
A:Cross-references: EMBL:X77317; NID:g452607; PIDN:CAA54523.1; PID:g452608
C:Superfamily: tumor necrosis factor
C:Keywords: cytokine; cyclooxin; glycoprotein; lymphokine; macrophage; membrane protein
F:42/Binding site: carbohydrate (Ser) (covalent) #status predicted
F:106-138/Disulfide bonds: #status predicted

Query Match      77.5%; Score 69; DB 1; Length 193;
Best Local Similarity 85.7%; Pred. No. 0.00044;
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 YSOVLFKGGCPST 14
Db 96 YSOVLFKGGCPST 109

RESULT 9
JH0529
tumor necrosis factor alpha precursor - sheep
N:Alternate names: cachectin; TNF alpha
C:Species: Ovis orientalis aries; Ovis ammon aries (domestic sheep)
C>Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 04-Feb-2000
C:Accession: JH0529; S48118; S13114; S20661
R:Green, I.R.; Sargan, D.R.
Gene 109, 203-210, 1991
A>Title: Sequence of the cDNA encoding ovine tumor necrosis factor-alpha: problems with
A:Reference number: JH0529; MUID:92112044; PMID:1765267
A:Accession: JH0529
A:Molecule type: mRNA
A:Residues: 1-234 <GRES>
A:Cross-references: EMBL:X55152; NID:g1405; PIDN:CAA38952.1; PID:g1406
R:Experimental source: alveolar macrophage
R:Nash, A.D.; Barcham, G.J.; Brandon, M.R.; Andrews, A.E.
Immunol. Cell Biol. 69, 273-283, 1991
A>Title: Molecular cloning, expression and characterization of ovine TNF-alpha.
A:Reference number: S48118; MUID:92155784; PMID:1786996
A:Accession: S48118
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-234 <NASS>
A:Cross-references: EMBL:X56756; NID:g297806; PIDN:CAA40076.1; PID:g297807
R:Young, A.J.; Hay, J.B.; Chan, J.Y.C.
Nucleic Acids Res. 18, 6723, 1990
A>Title: Primary structure of ovine tumor necrosis factor alpha cDNA.
A:Reference number: S13114; MUID:91067496; PMID:2251151
A:Accession: S13114
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-62, 64-234 <YOV>
A:Cross-references: EMBL:X55966; NID:g1403; PIDN:CAA39437.1; PID:g1404
A>Note: comparison with the introns of homologous sequences suggest that this is probably
C:Superfamily: tumor necrosis factor
C:Keywords: alternative splicing; cytokine; cyclooxin; glycoprotein; lipoprotein; lympho
F:1-77/poamain: propeptide #status predicted <PRO>
F:78-234/Product: tumor necrosis factor alpha #status predicted <TUM>
F:82/Binding site: myristate (Lys) (covalent) #status predicted
F:82/Binding site: carbohydrate (Ser) (covalent) #status predicted
F:96/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:146-178/Disulfide bonds: #status predicted

Query Match      77.5%; Score 69; DB 1; Length 234;
Best Local Similarity 85.7%; Pred. No. 0.00052;
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 YSOVLFKGGCPST 14

```

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Db 136 YSOVLFKGGCPST 149
|||||:| |||||
RESULT 10
QWMSN
tumor necrosis factor alpha precursor - mouse
N:Alternate names: cachectin; TNF alpha
C:Species: Mus musculus (house mouse)
C>Date: 31-Mar-1988 #sequence revision 31-Mar-1988 #text_change 04-Feb-2000
C:Accession: A22908; S03791; A27303; A25164; A23127; I59058; A36696
R:Shital, T.; Shimizu, N.; Shiojiri, S.; Horiguchi, S.; Ito, H.
DNA 7, 193-201, 1988
A>Title: Cloning and expression in Escherichia coli of the gene for mouse tumor necro
A:Reference number: A22908; MUID:88224564; PMID:2836146
A:Accession: A22908
A:Molecule type: DNA
A:Residues: 1-235 <SHI>
A:Cross-references: GB:M20155
R:Shakhov, A.N.; Nedospasov, S.A.
Bioorg. Khim. 13, 701-705, 1987
A>Title: Molecular cloning of the genes coding for tumor necrosis factors: complete n
A:Reference number: S03791; MUID:87298639; PMID:3040015
A:Accession: S03791
A:Molecule type: DNA
A:Residues: 1-235 <SHA>
A:Cross-references: GB:M38296; NID:g202086; PIDN:AAA40459.1; PID:g202087
A>Note: article in Russian with English abstract
R:Semun, D.; Kawashima, E.; Jongeneel, C.V.; Shakhov, A.N.; Nedospasov, S.A.
Nucleic Acids Res. 15, 9083-9084, 1987
A>Title: Nucleotide sequence of the murine TNF locus, including the TNF-alpha (tumor
A:Reference number: A36679; MUID:88067722; PMID:3684584
A:Accession: A27303
A:Molecule type: DNA
A:Residues: 1-235 <SEM>
A:Cross-references: GB:Y00467; NID:g54830; PIDN:CAA68530.1; PID:g54832
R:Penica, D.; Haylick, J.S.; Bringham, T.S.; Palladino, M.A.; Goeddel, D.V.
Proc. Natl. Acad. Sci. U.S.A. 82, 6060-6064, 1985
A>Title: Cloning and expression in Escherichia coli of the cDNA for murine tumor necr
A:Reference number: A25164; MUID:85298296; PMID:3898078
A:Accession: A25164
A:Molecule type: mRNA
A:Residues: 1-235 <PEN>
A:Cross-references: GB:M11731; NID:g202084; PIDN:AAA40458.1; PID:g202085
R:Fransen, L.; Muller, R.; Marmenout, A.; Tavernier, J.; van der Heyden, J.; Kawashim
Nucleic Acids Res. 13, 4417-4429, 1985
A>Title: Molecular cloning of mouse tumor necrosis factor cDNA and its eukaryotic ex
A:Reference number: A23127; MUID:85242112; PMID:2989794
A:Accession: A23127
A:Molecule type: mRNA
A:Residues: 1-235 <FRA>
A:Cross-references: GB:X02611; NID:g548444; PIDN:CAA26457.1; PID:g54845
R:Csch, K.; Beutler, B.
J. Biol. Chem. 264, 16256-16260, 1989
A>Title: Alternative cleavage of the cachectin/tumor necrosis factor propeptide resul
A:Reference number: A34251; MUID:89380231; PMID:2777790
A:Accession: A34251
A:Molecule type: protein
A:Residues: 70-87 <CSE>
R:Caput, D.; Beutler, B.; Hartog, K.; Thayer, R.; Brown-Shimer, S.L.; Cerami, A.
Proc. Natl. Acad. Sci. U.S.A. 83, 1670-1674, 1986
A>Title: Identification of a common nucleotide sequence in the 3'-untranslated region
A:Reference number: I59058; MUID:86149365; PMID:2419912
A:Accession: I59058
A:Status: Preliminary; translated from GB/EMBL/DBD
A:Molecule type: mRNA
A:Residues: 1-230, 'R', 232-235 <RES>
A:Cross-references: GB:M3049; NID:g202082; PIDN:AAA40457.1; PID:g202083
R:Sherry, B.; Jue, D.M.; Zentella, A.; Cerami, A.
Biochem. Biophys. Res. Commun. 173, 1072-1078, 1990
A>Title: Characterization of high molecular weight glycosylated forms of murine tumor
A:Reference number: A36696; MUID:91097531; PMID:2268312
A:Accession: A36696

```

A:Molecule type: protein
A:Residues: 80-85,'X',87-99 <SHE>
C:Genetics:
A:Introns: 62/3; 81/1; 97/1
A>Note: the first intron occurs in the 5'-untranslated region
C:Superfamily: tumor necrosis factor
C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; ment
F:80-235/Product: tumor necrosis factor #status experimental <MAT>
F:20/Binding site: myristate (lys) (covalent) #status predicted
F:84/Binding site: carbohydrate (Ser) (covalent) #status predicted
F:66/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:148-179/Disulfide bonds: #status predicted

Query Match 77.5%; Score 69; DB 1; Length 235;
Best Local Similarity 73.7%; Pred. No. 0.00053;
Matches 14; Conservative 0; Mismatches 1; Indels 4; Gaps 1;

OY 1 YSOVLFRGQGCPS---TH 15
Db 138 YSOVLFRGQGCPSVLLTH 156

RESULT 11

JU0029
tumor necrosis factor alpha precursor - rat
N:Alternate names: cachectin; TNF alpha
C:Species: Rattus norvegicus (Norway rat)
C>Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 04-Feb-2000
C:Accession: JU0029; JN0868; S21674
R:Shirai, T.; Shimizu, N.; Horiguchi, S.; Ito, H.
Agric. Biol. Chem. 53, 1733-1736, 1989
A:Title: Cloning and expression in Escherichia coli of the gene for rat tumor necrosis f
A:Reference number: JU0029

A:Molecule type: DNA
A:Residues: 1-235 <SHI>
R:Kwon, J.; Chung, I.Y.; Benveniste, E.N.
Gene 132, 227-236, 1993
A:Title: Cloning and sequence analysis of the rat tumor necrosis factor-encoding genes.
A:Reference number: JN0868; MUID:94040766; PMID:8224868
A:Accession: JN0868

A:Molecule type: DNA
A:Residues: 1-235 <KWO>
A:Cross-references: GB:I00981; NID:g205253; PIDN:AAA16275.1; PID:g205254
R:Estler, H.C.; Grewe, M.; Gausling, R.; Pavlovic, M.; Decker, K.
Biol. Chem. Hoppe-Seyler 373, 271-281, 1992
A:Title: Rat tumor necrosis factor- α transcription in rat Kupffer cells and in vitr
A:Reference number: S21674; MUID:92329007; PMID:1627266
A:Accession: S21674

A:Molecule type: mRNA
A:Residues: 1-38, 'P',40-162,'T',164-201,'S',203-235 <RST>
A:Cross-references: GB:X66539; GB:S40199; NID:g395369; PIDN:CAA47146.1; PID:g395370
C:Comment: Tumor necrosis factor is secreted by macrophages in response to endotoxin and
C:Genetics:

A:Gene: TNF- α
A:Introns: 62/3; 81/1; 97/1
C:Superfamily: tumor necrosis factor
C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; ment
F:80-235/Product: tumor necrosis factor #status predicted <MAT>
F:19,20/Binding site: myristate (lys) (covalent) #status predicted
F:84/Binding site: carbohydrate (Ser) (covalent) #status predicted
F:66/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:148-179/Disulfide bonds: #status predicted

Query Match 77.5%; Score 69; DB 2; Length 235;
Best Local Similarity 73.7%; Pred. No. 0.00053;
Matches 14; Conservative 0; Mismatches 1; Indels 4; Gaps 1;

OY 1 YSOVLFRGQGCPS---TH 15
Db 138 YSOVLFRGQGCPSVLLTH 156

RESULT 12

I54490
tumor necrosis factor alpha precursor - white-footed mouse
C:Species: Peromyscus leucopus (white-footed mouse)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 04-Feb-2000
C:Accession: I54490
R:Crew, M.D.; Filipowsky, M.E.
Immunogenetics 35, 351-353, 1992

A:Title: Sequence of the tumor necrosis factor/cachectin (TNF) gene from Peromyscus 1
A:Reference number: I54490; MUID:92218012; PMID:1348497
A:Accession: I54490

A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-235 <RES>
A:Cross-references: GB:M59233; NID:g202506; PIDN:AAA40596.1; PID:g202507
C:Genetics:

A:Gene: lTNF
A:Introns: 62/3; 81/1; 97/1
C:Superfamily: tumor necrosis factor
C:Keywords: glycoprotein; lipoprotein; myristylation
F:19,20/Binding site: myristate (lys) (covalent) #status predicted
F:84/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 73.0%; Score 65; DB 2; Length 235;
Best Local Similarity 73.7%; Pred. No. 0.0025;
Matches 14; Conservative 0; Mismatches 1; Indels 4; Gaps 1;

OY 1 YSOVLFRGQGCPS---TH 15
Db 138 YSOVLFRGQGCSSVLLTH 156

RESULT 13

A25451
tumor necrosis factor alpha precursor - rabbit

N:Alternate names: cachectin; TNF alpha
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C:Accession: A25454; A25451; J50727
R:Ito, H.; Yamamoto, S.; Kuroda, S.; Sakamoto, H.; Kajihara, J.; Kiyota, T.; Hayashi,
DNA 5, 149-156, 1986

A:Title: Molecular cloning and expression in Escherichia coli of the cDNA coding for
A:Reference number: A25454; MUID:86219711; PMID:3519137
A:Accession: A25454

A:Molecule type: mRNA
A:Residues: 1-234 <ITO>
A:Cross-references: GB:M12845; NID:g165759; PIDN:AAA31486.1; PID:g165760
R:Ito, H.; Shirai, T.; Yamamoto, S.; Akira, M.; Kawahara, S.; Todd, C.W.; Wallace, R.
DNA 5, 157-165, 1986

A:Title: Molecular cloning of the gene encoding rabbit tumor necrosis factor.
A:Reference number: A25451; MUID:86219712; PMID:3519138
A:Accession: A25451
A:Molecule type: DNA
A:Residues: 1-234 <ITO>

A>Note: this sequence differs from that shown in having a Gln inserted between residu
R:Shahov, A.N.; Kuprash, D.V.; Aizov, M.M.; Jongeneel, C.V.; Nedospasov, S.A.
Gene 95, 215-221, 1990

A:Title: Structural analysis of the rabbit TNF locus, containing the genes encoding T
A:Reference number: JH0309; MUID:91065534; PMID:2249779
A:Accession: J50727
A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
A:Residues: 1-62,'Q',63-234 <SHA>
A:Cross-references: GB:M60340; GB:M53526; NID:g165754; PIDN:AAA31484.1; PID:g165756
C:Genetics:

A:Introns: 62/3; 80/1; 96/1
C:Superfamily: tumor necrosis factor
C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; m
F:1-81/Domain: propeptide #status predicted <PRO>
F:82-234/Product: tumor necrosis factor #status predicted <MAT>
F:19,20/Binding site: myristate (lys) (covalent) #status predicted
F:83/Binding site: carbohydrate (Ser) (covalent) #status predicted
F:147-178/Disulfide bonds: #status predicted

Query Match 66.3%; Score 59; DB 1; Length 234;
 Best Local Similarity 68.4%; Pred. No. 0.025;
 Matches 13; Conservative 0; Mismatches 2; Indels 4; Gaps 1;

OY 1 YSOVLFKGGGCS---TH 15
 ||||| ||||| ||
 DB 137 YSOVLFSGGGCRSYVLTH 155

RESULT 14

tumor necrosis factor beta precursor - rabbit
 JH0309

N:Alternate names: lymphotoxin; TNF beta

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: JH0309; PN0098

R:Shakhov, A.N.; Kuprash, D.V.; Azizov, M.M.; Jongeneel, C.V.; Nedospasov, S.A.

Gene 95, 215-221, 1990

A:Title: Structural analysis of the rabbit TNF locus, containing the genes encoding TNF-

A:Reference number: JH0309; MUID:91065534; PMID:2249779

A:Accession: JH0309

A:Molecule type: DNA

A:Residues: 1-197 <SH2>

A:Cross-references: GB:M60340; GB:M35326; NID:g165754; PIDN:AAA31483.1; PID:g165755; GB:

R:Shakhov, A.N.; Kuprash, D.V.; Turetskaya, R.L.; Azizov, M.M.; Andreyeva, A.V.; Nedospa

Mol. Biol. (Mosk.) 23, 1743-1750, 1989

A:Title: Cloning and structural analysis of the genes, coding for rabbit tumor necrosis

A:Reference number: PN0098; MUID:90220566; PMID:2633043

A:Accession: PN0098

A:Molecule type: mRNA

A:Residues: 1-197 <SHA>

A:Cross-references: GB:X55745; NID:g297167; PIDN:CAA39275.1; PID:g297168

C:Genetics:

A:introns: 25/3; 61/1

C:Superfamily: tumor necrosis factor

C:Keywords: cytokine; cytotoxin; glycoprotein; lymphokine; macrophage

F:1-26/Domain: signal sequence #status predicted <SIG>

F:27-197/Product: lymphotoxin #status predicted <MAT>

Query Match

Best Local Similarity 56.2%; Score 50; DB 1; Length 197;

Best Local Similarity 72.7%; Pred. No. 0.68;

Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 YSOVLFKGGGC 11
 ||||| :|||
 DB 102 YSOVVFSGGEC 112

RESULT 15

S17289

tumor necrosis factor beta precursor - pig

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: S17289

R:Kuhner, P.; Wuehrich, C.; Peterhans, E.; Pauli, U.

Gene 102, 171-178, 1991

A:Title: The porcine tumor necrosis factor-encoding genes: sequence and comparative anal

A:Reference number: S17289; MUID:91340150; PMID:1874444

A:Accession: S17289

A:Molecule type: DNA

A:Residues: 1-204 <RUH>

A:Cross-references: EMBL:X54859; NID:g2132; PIDN:CAA38638.1; PID:g2133

C:Genetics:

A:introns: 32/3; 68/1

C:Superfamily: tumor necrosis factor

C:Keywords: cytokine; cytotoxin; glycoprotein; lymphokine; macrophage

F:1-33/Domain: signal sequence #status predicted <SIG>

F:34-204/Product: tumor necrosis factor beta #status predicted <MAT>

Query Match

Best Local Similarity 56.2%; Score 50; DB 1; Length 204;

Best Local Similarity 72.7%; Pred. No. 0.7;

Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 YSOVLFKGGGC 11
 ||||| :|||
 DB 109 YSOVVFSGGEC 119

Search completed: December 4, 2002, 13:25:03
 Job time : 12.3684 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 4, 2002, 13:18:33 ; Search time 6.31579 Seconds
(without alignments)
105.073 Million cell updates/sec

Title: US-09-754-004-1
Perfect score: 89
Sequence: 1 YSQLFKGCGCPSTHV 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_40:*
Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	89	100.0	233	1	TNFA_CANFA
2	89	100.0	233	1	TNFA_HUMAN
3	89	100.0	233	1	TNFA_PAPSE
4	89	100.0	234	1	TNFA_HORSE
5	84	94.4	233	1	TNFA_MACFA
6	84	94.4	233	1	TNFA_MACMU
7	84	94.4	233	1	TNFA_PAPHU
8	83	93.3	233	1	TNFA_DELE
9	83	93.3	233	1	TNFA_FELCA
10	83	93.3	233	1	TNFA_TURTR
11	79	88.8	232	1	TNFA_PIG
12	74	83.1	233	1	TNFA_BOVIN
13	73	82.0	233	1	TNFA_MARMO
14	73	82.0	234	1	TNFA_CAVPO
15	69	77.5	234	1	TNFA_SHEEP
16	69	77.5	234	1	TNFA_MOUSE
17	69	77.5	235	1	TNFA_MOUSE
18	69	77.5	235	1	TNFA_MOUSE
19	68	76.4	229	1	TNFA_CEREL
20	65	73.0	235	1	TNFA_PERLE
21	59	66.3	235	1	TNFA_RABIT
22	54	60.7	205	1	TNFA_MARMO
23	50	56.2	197	1	TNFA_RABIT
24	50	56.2	204	1	TNFA_PIG
25	49	55.1	204	1	TNFA_BOVIN
26	48.5	54.5	233	1	TNFA_MACEU
27	45.5	51.1	278	1	TNFA_RAT
28	45.5	51.1	280	1	TNFA_CERTO
29	45.5	51.1	280	1	TNFA_MACMU
30	45.5	51.1	281	1	TNFA_HUMAN
31	45	50.6	360	1	TNFA_MOUSE
32	44.5	50.0	279	1	TNFA_MOUSE
33	44	49.4	202	1	TNFA_MOUSE

34	44	49.4	202	1	TNFA_RAT	006332 rattus norv
35	43	48.3	104	1	C551_PSEAE	P00099 pseudomona
36	42.5	47.8	282	1	TNFA_PIG	Q06888 sus scrofa
37	42	47.2	233	1	TNFA_TRIVU	P79374 trichosurus
38	41	46.1	201	1	TNFA_MACEU	Q91478 macropus eu
39	41	46.1	791	1	G6PE_HUMAN	O95479 homo sapien
40	40	44.9	109	1	S213_MOUSE	O55038 mus musculu
41	40	44.9	239	1	TN14_MOUSE	O99y98 mus musculu
42	39	43.8	109	1	S213_HUMAN	O43927 homo sapien
43	39	43.8	521	1	SPKA_STY13	Q9fab3 synechocyst
44	39	43.8	1295	1	BXAL_CLOBO	P10845 clostridium
45	38.5	43.3	282	1	YIAL_ECOLI	P37671 escherichia

ALIGNMENTS

RESULT 1
TNFA_CANFA STANDARD: PRT: 233 AA.
AC P51742: 028339;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
ligand superfamily member 2) (Cachectin).
GN TNF OR TNFSF2 OR TNFA.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxID=9615;
RX [1]
RP SEQUENCE FROM N.A.
RA Fiers W., Beernaert M.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Zucker K., Lu P., Fuller L., Asthana D., Esquenazi V., Miller J.;
RT "Cloning and expression of the cDNA for canine tumor necrosis
factor-alpha in E. coli.";
RL Lymphokine Res. 13:191-196(1994).
RN [3]
RP SEQUENCE OF 74-205 FROM N.A.
RA SPRAIN-BEAGLE; TISSUE=Blood;
RC Gilmore W.H., Carter S.D., Bennett M., Barnes A., Kelly D.F.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: cytokine that binds to TNFRSF1A/TNFR1 and
TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
induce cell death of certain tumor cell lines. It is potent
pyrogen causing fever by direct action or by stimulation of
interleukin 1 secretion and is implicated in the induction of
cachexia. Under certain conditions it can stimulate cell
proliferation and induce cell differentiation.
CC -1- SUBUNIT: Homotrimer (by similarity).
CC -1- SUBCELLULAR LOCATION: Type II MEMBRANE PROTEIN. ALSO EXISTS AS AN
EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).
CC -1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
PROTEOLYTIC PROCESSING (BY SIMILARITY).
CC -1- PTM: The membrane form, but not the soluble form, is
phosphorylated on serine residues. Dephosphorylation of the
membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (by
similarity).
CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
AND MALNUTRITION.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
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CC or send an email to license@isb-sib.ch).

DR EMBL: X94932; CAA64403.1; -

DR EMBL: S74068; AAB32391.1; -

DR EMBL: Z70046; CAA93908.1; -

DR HSSP: P01375; 4TSV

DR InterPro: IPR003636; TNF_family.

DR InterPro: IPR000478; TNF_family.

DR Pfam: PF00229; TNF; 1.

DR PRINTS: PR01234; TNECROSISFCT.

DR PRODOM: PD002012; TNF_abc; 1.

DR SMART: SM00207; TNF; 1.

DR PROSITE: PS00251; TNF_1; 1.

DR PROSITE: PS0049; TNF_2; 1.

KW Cytokine; Cytotoxin; Transmembrane; Phosphorylation; Signal-anchor.

FT CHAIN 1 233 TUMOR NECROSIS FACTOR, MEMBRANE FORM.

FT DOMAIN 77 233 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).

FT DOMAIN 57 233 EXTRACELLULAR (POTENTIAL).

FT SITE 76 77 CLEAVAGE (BY ADAM17) (BY SIMILARITY).

FT MOD_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).

FT DISULFID 145 177 BY SIMILARITY.

FT CONFLICT 59 60 OR -> PE (IN REF. 2).

FT CONFLICT 66 66 A -> C (IN REF. 2).

FT CONFLICT 74 74 A -> V (IN REF. 3).

FT CONFLICT 111 111 A -> D (IN REF. 2).

FT CONFLICT 116 116 G -> D (IN REF. 2).

FT CONFLICT 134 135 IY -> DS (IN REF. 2).

SO SEQUENCE 233 AA; 25447 MW; 7B2588BFC8B2340 CRC64;

Query Match Best Local Similarity 100.0%; Score 89; DB 1; Length 233; Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YSOVLFKSGGCPSTHV 16

DB 135 YSOVLFKSGGCPSTHV 150

RESULT 2

TNFA_HUMAN

ID	TNFA_HUMAN	STANDARD:	PRT:	233 AA.
AC	P01375;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor ligand superfamily member 2) (Cachectin).			
GN	TNF OR TNFSF2 OR TNFA.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=87217060; PubMed=3555974;			
RA	Nedosposov S.A., Shakhov A.N., Turetskaya R.L., Mett V.A.,			
RA	Azizov M.M., Georgiev G.P., Korobko V.G., Dobrynin V.N.,			
RA	Filipov S.A., Bystrov N.S., Boldyreva E.F., Chuvpilo S.A.,			
RA	Chumakov A.M., Shingarova L.N., Ovchinnikov Y.A.;			
RT	"Tandem arrangement of genes coding for tumor necrosis factor (TNF-alpha) and lymphotoxin (TNF-beta) in the human genome.;"			
RL	Cold Spring Harb. Symp. Quant. Biol. 51:611-624(1986).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=85086244; PubMed=6392892;			
RA	Pennica D., Nedwin G.E., Haylic J.S., Seeburg P.H., Derynck R.,			
RA	Palladino M.A., Kohr W.J., Aggarwal B.B., Goeddel D.V.;			
RT	"Human tumour necrosis factor: precursor, structure, expression and			
RL	homology to lymphotoxin.;"			
RL	Nature 312:724-729(1984).			

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=85137898; PubMed=3883195;

RA Shirai T., Yamaguchi H., Ito H., Todd C.W., Wallace R.B.;

RT "Cloning and expression in *Escherichia coli* of the gene for human

RT tumour necrosis factor.;"

RL Nature 313:803-806(1985).

RN [4]

RP SEQUENCE FROM N.A.

RX MEDLINE=86016093; PubMed=2995927;

RA Nedwin G.E., Naylor S.L., Sakaguchi A.Y., Smith D.H.,

RA Jarrett-Nedwin J., Pennica D., Goeddel D.V., Gray P.W.;

RT "Human lymphotoxin and tumor necrosis factor genes: structure,

RT homology and chromosomal localization.;"

RL Nucleic Acids Res. 13:6361-6373(1985).

RN [5]

RP SEQUENCE FROM N.A.

RX MEDLINE=85142190; PubMed=3856324;

RA Wang A.M., Creasey A.A., Ladner M.B., Lin L.S., Strickler J.,

RA van Arsdel J.N., Yamamoto R., Mark D.F.;

RT "Molecular cloning of the complementary DNA for human tumor necrosis

RT factor.;"

RL Science 228:149-154(1985).

RN [6]

RP SEQUENCE FROM N.A.

RX MEDLINE=86030296; PubMed=3932069;

RA Marmenout A., Fransen L., Tavernier J., van der Heyden J., Tizard R.,

RA Kawashima E., Shaw M., Johnson M.J., Semon D., Mueller R.,

RA Ruysschaert M.R., van Vliet A., Fiers W.;

RT "Molecular cloning and expression of human tumor necrosis factor and

RT comparison with mouse tumor necrosis factor.;"

RL Eur. J. Biochem. 152:515-522(1985).

RN [7]

RP SEQUENCE FROM N.A.

RX MEDLINE=93272029; PubMed=8499947;

RA Irits F.J.M., Bougueleret L., Prieur S., Caterina D., Primas G.,

RA Perrot V., Jurka J., Rodriguez-Tome P., Claverie J.-M., Dausset J.,

RA Cohen D.;

RT "Dense Alu clustering and a potential new member of the NF kappa B

RT family within a 90 kilobase HLA class III segment.;"

RL Nat. Genet. 3:137-145(1993).

RN [8]

RP SEQUENCE FROM N.A.

RX Rowen L., Madan A., Qin S., Shaffer T., James R., Ratcliffe A.,

RA Abbasi N., Dickhoff R., Loretz C., Madan A., Dors M., Young J.,

RA Lasky S., Hood L.;

RT "Sequence of the human major histocompatibility complex class III

RT region.;"

RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.

RN [9]

RP SEQUENCE FROM N.A.

RX Shina S., Tamiya G., Oka A., Inoko H.;

RT "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region.;"

RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

RN [10]

RP SEQUENCE FROM N.A.

RX Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Yi Q.,

RA Nickerson D.A.;

RT Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

RN [11]

RP SEQUENCE FROM N.A.

RX Straussberg R.;

RT Tissue-Blood;

RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

RN [12]

RP PHOSPHORYLATION (MEMBRANE FORM).

RX PubMed=8597870;

RA Pocsik E., Duda E., Wallach D.;

RT "Phosphorylation of the 26 kDa TNF precursor in monocytic cells and in

RL transfected HeLa cells.;"

RL J. Inflamm. 45:152-160(1995).

RN [13]

RP PHOSPHORYLATION BY CK1, AND DEPHOSPHORYLATION.

RX PubMed-10205166;
 RA Watts A.D., Hunt N.H., Maniasekara Y., Bloomfield G., Wallach D.,
 RA Roufogalis B.D., Chaudhri G.;
 RT "A casein kinase I motif present in the cytoplasmic domain of members
 RT of the tumor necrosis factor ligand family is implicated in 'reverse
 RT signalling'.";
 RL EMBO J. 18:2119-2126(1999).
 RN [14]
 RP MUTAGENESIS.
 RX MEDLINE-91184128; PubMed-2009860;
 RA Ostad X.V., Tavernier J., Prange T., Fiers W.;
 RT "Localization of the active site of human tumour necrosis factor
 RT (TNF) by mutational analysis.";
 RL EMBO J. 10:827-836(1991).
 RN [15]
 RP MISTRIOYLATION.
 RX MEDLINE-93018820; PubMed-1402651;
 RA Stevenson F.T., Bursten S.L., Locksley R.M., Lovett D.H.;
 RT "Myristyl acylation of the tumor necrosis factor alpha precursor on
 RT specific lysine residues.";
 RL J. Exp. Med. 176:1053-1062(1992).
 RN [16]
 RP CLEAVAGE BY ADAM17.
 RX MEDLINE-97166575; PubMed-9034191;
 RA Moss M.L., Jin S.-L.C., Milla M.E., Burkhart W., Carter H.L.,
 RA Chen W.-J., Clay W.C., Didsbury J.R., Hassler D., Hoffman C.R.,
 RA Kost T.A., Lambert M.H., Leesnitzer M.A., McCauley P., McGehee G.,
 RA Mitchell J., Moyer M., Patel G., Rocque W., Overton L.K., Schoenen F.,
 RA Sason T., Su J.-L., Warner J., Willard D., Becherer J.D.;
 RT "Cloning of a disintegrin metalloproteinase that processes precursor
 RT tumour-necrosis factor-alpha.";
 RL Nature 385:733-736(1997).
 RN [17]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX MEDLINE-89159409; PubMed-2922050;
 RA Jones E.Y., Stuart D.I., Walker N.P.;
 RT "Structure of tumour necrosis factor.";
 RL Nature 338:225-228(1989).
 RN [18]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX MEDLINE-91193276; PubMed-1964681;
 RA Jones E.Y., Stuart D.I., Walker N.P.;
 RT "The structure of tumour necrosis factor -- implications for
 RT biological function.";
 RL J. Cell Sci. Suppl. 13:11-18(1990).
 RN [19]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
 RX MEDLINE-90008932; PubMed-2551905;
 RA Eck M.J., Sprang S.R.;
 RT "The structure of tumor necrosis factor-alpha at 2.6-A resolution.
 RT Implications for receptor binding.";
 RL J. Biol. Chem. 264:11795-11805(1989).
 RN [20]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF MUTANT ARG-107.
 RX MEDLINE-98147459; PubMed-9488135;
 RA Reed C., Fu Z.Q., Wu J., Xue Y.N., Harrison R.W., Chen M.J.,
 RA Weber I.T.;
 RT "Crystal structure of TNF-alpha mutant R31D with greater affinity for
 RT receptor R1 compared with R2.";
 RL Protein Eng. 10:1101-1107(1997).
 RN [21]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF MUTANT M3S.
 RX MEDLINE-98113178; PubMed-9442056;
 RA Cha S.S., Kim J.S., Cho H.S., Shin N.K., Jeong W., Shin H.C.,
 RA Kim Y.J., Hahn J.H., Oh B.H.;
 RT "High resolution crystal structure of a human tumor necrosis factor-
 RT alpha mutant with low systemic toxicity.";
 RL J. Biol. Chem. 273:2153-2160(1998).
 CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
 CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
 CC induce cell death of certain tumor cell lines. It is potent
 CC pyrogen causing fever by direct action or by stimulation of
 CC interleukin 1 secretion and is implicated in the induction of

CC cachexia, under certain conditions it can stimulate cell
 CC proliferation and induce cell differentiation.
 CC -1- SUBUNIT: Homotrimer.
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
 CC EXTRACELLULAR SOLUBLE FORM.
 CC -1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
 CC PROTEOLYTIC PROCESSING.
 CC -1- PTM: The membrane form, but not the soluble form, is
 CC phosphorylated on serine residues. Dephosphorylation of the
 CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1.
 CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
 CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
 CC AND MALNUTRITION.
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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 CC -----
 DR EMBL: X02910; CAA26669.1; -
 Query Match 100.0%; Score 89; DB 1; Length 233;
 Best Local Similarity 100.0%; Pred. No. 5,3e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YSQVLFKGGCGPSTHV 16
 Db 135 YSQVLFKGGCGPSTHV 150
 |||||
 RESULT 3
 TNFA_PAPSP STANDARD; PRT; 233 AA.
 AC P33620;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor precursor (TNF-alpha) ("Tumor necrosis factor
 DE ligand superfamily member 2) (Cachectin).
 GN TNF OR TNFSF2 OR TNFA.
 OS Papio sp. (baboon).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Papio.
 OX NCBI_TaxID=61183;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sanjanwal M., Edwards A.;
 RL submitted (SEP-1991) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
 CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
 CC induce cell death of certain tumor cell lines. It is potent
 CC pyrogen causing fever by direct action or by stimulation of
 CC interleukin 1 secretion and is implicated in the induction of
 CC cachexia. Under certain conditions it can stimulate cell
 CC proliferation and induce cell differentiation.
 CC -1- SUBUNIT: Homotrimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
 CC extracellular soluble form (By similarity).
 CC -1- PTM: The soluble form derives from the membrane form by
 CC proteolytic processing (By similarity).
 CC -1- PTM: The membrane form, but not the soluble form, is
 CC phosphorylated on serine residues. Dephosphorylation of the
 CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
 CC similarity).
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
 CC -----
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CC -----
 DR EMBL: X62141; CAA44068.1; -
 DR PIR: S22052; S22052.
 DR HSSP: P01375; 1A8M.
 DR InterPro: IPR003636; TNF_abc.
 DR InterPro: IPR000478; TNF_family.
 DR Pfam: PF00229; TNF; 1.
 DR PRINTS: PR01234; TNECROSISFCT.
 DR PRODOM: PD002012; TNF_abc; 1.
 DR SMART: SM00207; TNF; 1.
 DR PROSITE: PS00251; TNF_1; 1.
 DR PROSITE: PS50049; TNF_2; 1.
 DR Cytokine; Cytotoxin; Transmembrane; Phosphorylation; Signal-anchor;
 KW Myristate.
 FT CHAIN 1 233 TUMOR NECROSIS FACTOR, MEMBRANE FORM.
 FT CHAIN 77 233 TUMOR NECROSIS FACTOR, SOLUBLE FORM.
 FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT DOMAIN 57 233 EXTRACELLULAR (POTENTIAL).
 FT SITE 76 77 CLEAVAGE (BY ADAM17) (BY SIMILARITY).
 FT MOD_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
 FT LIPID 19 19 MYRISTATE (BY SIMILARITY).
 FT LIPID 20 20 MYRISTATE (BY SIMILARITY).
 FT DISULFID 145 177 BY SIMILARITY.
 FT SEQUENCE 233 AA; 25557 MW; 455360B48DC74173 CRC64;

Query Match 100.0%; Score 89; DB 1; Length 233;
 Best Local Similarity 100.0%; Pred. No. 5.3e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YSOVLFKGGCGPSTHY 16
 DB 135 YSOVLFKGGCGPSTHY 150
 ||||||||||||||||

RESULT 4
 TNFA_HORSE STANDARD; PRT; 234 AA.
 ID TNFA_HORSE
 AC P29553;
 DT 01-APR-1993 (Rel. 25; Created)
 DT 01-APR-1993 (Rel. 25; Last sequence update)
 DT 15-JUN-2002 (Rel. 41; Last annotation update)
 DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
 DE ligand superfamily member 2) (Cachectin).
 GN TNF OR TNFSF2 OR TNFA.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_Taxid=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92084125; PubMed=1748301;
 RA Su X., Morris D.D., McGraw R.A.;
 RT "Cloning and characterization of gene TNF alpha encoding equine tumor
 RT necrosis factor alpha."
 RL Gene 107:319-321(1991).
 CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
 CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
 CC induce cell death of certain tumor cell lines. It is potent
 CC pyrogen causing fever by direct action or by stimulation of
 CC interleukin 1 secretion and is implicated in the induction of
 CC cachexia. Under certain conditions it can stimulate cell
 CC proliferation and induce cell differentiation.
 CC -1- SUBUNIT: Homotrimer (by similarity).
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
 CC extracellular soluble form (by similarity).
 CC -1- PPM: The soluble form derives from the membrane form by

CC proteolytic processing (by similarity).
 CC -1- PPM: The membrane form, but not the soluble form, is
 CC phosphorylated on serine residues. Dephosphorylation of the
 CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (by
 CC similarity).
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

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CC EMBL: M64087; AAA30959.1; -
 DR PIR: J01344; J01344.
 DR HSSP: P01375; 1A8M.
 DR InterPro: IPR003636; TNF_abc.
 DR InterPro: IPR000478; TNF_family.
 DR Pfam: PF00229; TNF; 1.
 DR PRINTS: PR01234; TNECROSISFCT.
 DR PRODOM: PD002012; TNF_abc; 1.
 DR SMART: SM00207; TNF; 1.
 DR PROSITE: PS00251; TNF_1; 1.
 DR PROSITE: PS50049; TNF_2; 1.
 DR Cytokine; Cytotoxin; Transmembrane; Phosphorylation; Signal-anchor.
 KW CHAIN 1 234 TUMOR NECROSIS FACTOR, MEMBRANE FORM.
 FT CHAIN 78 234 TUMOR NECROSIS FACTOR, SOLUBLE FORM.
 FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT DOMAIN 57 234 EXTRACELLULAR (POTENTIAL).
 FT SITE 77 78 CLEAVAGE (BY ADAM17) (BY SIMILARITY).
 FT MOD_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
 FT DISULFID 146 178 BY SIMILARITY.
 FT SEQUENCE 234 AA; 25469 MW; E79ACE91143DF373 CRC64;

Query Match 100.0%; Score 89; DB 1; Length 234;
 Best Local Similarity 100.0%; Pred. No. 5.3e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YSOVLFKGGCGPSTHY 16
 DB 136 YSOVLFKGGCGPSTHY 151
 ||||||||||||||||

RESULT 5
 TNFA_MACFA STANDARD; PRT; 233 AA.
 ID TNFA_MACFA
 AC P79337;
 DT 15-JUL-1998 (Rel. 36; Created)
 DT 15-JUL-1998 (Rel. 36; Last sequence update)
 DT 15-JUN-2002 (Rel. 41; Last annotation update)
 DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
 DE ligand superfamily member 2) (Cachectin).
 GN TNF OR TNFSF2 OR TNFA.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_Taxid=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Lymphocytes;
 RA Tatsumi M.;
 RT Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
 CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
 CC induce cell death of certain tumor cell lines. It is potent
 CC pyrogen causing fever by direct action or by stimulation of
 CC interleukin 1 secretion and is implicated in the induction of
 CC cachexia. Under certain conditions it can stimulate cell

```

CC proliferation and induce cell differentiation.
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC extracellular soluble form (By similarity).
CC -1- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -1- PTM: The membrane form, but not the soluble form, is
CC phosphorylated on serine residues. Dephosphorylation of the
CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC similarity).
CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC AND MALNUTRITION.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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CC -----
DR EMBL; AB000513; BAA19131.1; -.
DR HSSP; P01375; ATSV.
DR InterPro: IPR003636; TNF_abc.
DR InterPro: IPR000478; TNF_family.
DR Pfam; PF00228; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR PRODOM; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
DR Cytochrome; Cytochrome; Transmembrane; Phosphorylation; Signal-anchor.
KW CHAIN 1 233
FT CHAIN 1 233
FT CHAIN 77 233
FT CHAIN 1 35
FT TRANSMEM 36 56
FT TRANSMEM 36 56
FT DOMAIN 57 233
FT SITE 76 77
FT MOD_RES 2 2
FT DISULFD 145 177
SQ SEQUENCE 233 AA; 25558 MW; 6ABF2C3AB132C217 CRC64;

Query Match 94.4%; Score 84; DB 1; Length 233;
Best Local Similarity 93.8%; Pred. No. 3.7e-07;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 YSOVLFKGGGCPSTHY 16
Db 135 YSOVLFKGGGCPSTHY 150

RESULT 6
TNFA_MACMU STANDARD: PRT; 233 AA.
AC P48094;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE ligand superfamily member 2) (Cachectin).
GN TNF OR TNFSF2 OR TNFA.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96003435; PubMed=7561102;
RA Villinger F.J., Brat S.S., Mayne A.E., Chikkala N., Ansari A.A.;

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RP "Comparative sequence analysis of cytokine genes from human and
RP nonhuman primates."
RL J. Immunol. 155:3946-3954(1995).
CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC TNFRSF1B/TNFR2. It is mainly secreted by macrophages and can
CC induce cell death of certain tumor cell lines. It is potent
CC pyrogen causing fever by direct action or by stimulation of
CC interleukin 1 secretion and is implicated in the induction of
CC cachexia, under certain conditions it can stimulate cell
CC proliferation and induce cell differentiation.
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC extracellular soluble form (By similarity).
CC -1- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -1- PTM: The membrane form, but not the soluble form, is
CC phosphorylated on serine residues. Dephosphorylation of the
CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC similarity).
CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC AND MALNUTRITION.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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CC -----
DR EMBL; U19850; AAA86712.1; -.
DR HSSP; P01375; ATSV.
DR InterPro: IPR003636; TNF_abc.
DR InterPro: IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR PRODOM; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
KW Cytokine; Cytochrome; Transmembrane; Phosphorylation; Signal-anchor.
KW CHAIN 1 233
FT CHAIN 1 233
FT CHAIN 77 233
FT CHAIN 1 35
FT TRANSMEM 36 56
FT TRANSMEM 36 56
FT DOMAIN 57 233
FT SITE 76 77
FT MOD_RES 2 2
FT DISULFD 145 177
SQ SEQUENCE 233 AA; 25630 MW; 9F6F85050595FD59 CRC64;

Query Match 94.4%; Score 84; DB 1; Length 233;
Best Local Similarity 93.8%; Pred. No. 3.7e-07;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 YSOVLFKGGGCPSTHY 16
Db 135 YSOVLFKGGGCPSTHY 150

RESULT 7
TNFA_PAPHU STANDARD: PRT; 233 AA.
AC O7510;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE ligand superfamily member 2) (Cachectin).
GN TNF OR TNFSF2 OR TNFA.

```

OS Papio hamadryas ursinus (Chacma baboon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Papio.
 OX NCBI_TaxID=36229;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=98147379; PubMed=9488055;
 RA Haudek S.B., Redl H., Schlag G., Giroir B.P.,
 RT "Complementary DNA (cDNA) sequence of baboon tumor necrosis factor
 RT alpha."
 RL Mol. Immunol. 34:1041-1042(1997).
 CC -I- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
 CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
 CC induce cell death of certain tumor cell lines. It is potent
 CC pyrogen causing fever by direct action or by stimulation of
 CC interleukin 1 secretion and is implicated in the induction of
 CC cachexia, under certain conditions it can stimulate cell
 CC proliferation and induce cell differentiation.
 CC -I- SUBUNIT: Homotrimer (By similarity).
 CC -I- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
 CC extracellular soluble form (By similarity).
 CC -I- PTM: The soluble form derives from the membrane form by
 CC proteolytic processing (By similarity).
 CC -I- PTM: The membrane form, but not the soluble form, is
 CC phosphorylated on serine residues. Dephosphorylation of the
 CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
 CC similarity).
 CC -I- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
 CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
 CC AND MALNUTRITION.
 CC -I- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AF019963; AAC31675.1; -.
 CC HSSP: P01375; 4TSV.
 CC InterPro: IPR003636; TNF_abc.
 CC InterPro: IPR000478; TNF_family.
 CC Pfam: PF00229; TNF_1.
 CC PRINTS: PR01234; TNECROSISFCT.
 CC PRODOM: PD002012; TNF_abc; 1.
 CC SMART: SM00207; TNF; 1.
 CC PROSITE: PS00251; TNF_1; 1.
 CC PROSITE: PS50049; TNF_2; 1.
 CC DR Cytokine; Cytotoxin; Transmembrane; Phosphorylation; Signal-anchor.
 CC KW CHAIN 1 233
 CC FT CHAIN 1 233
 CC FT DOMAIN 1 35
 CC FT TRANSMEM 36 56
 CC FT SIGNAL-ANCHOR (POTENTIAL).
 CC FT CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 36 56
 CC FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 CC FT DOMAIN 57 233
 CC FT SITE 76 77
 CC FT MOD_RES 2 2
 CC FT DISULFID 145 177
 CC FT CARBOHYD 95 95
 CC FT N-LINKED (GLCNAC...) (POTENTIAL).
 CC SO SEQUENCE 233 AA; 25658 MW; B9403255058DA03 CRC64;
 CC
 CC Query Match 94.4%; Score 84; DB 1; Length 233;
 CC Best Local Similarity 93.8%; Pred. No. 3.7e-07;
 CC Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

TNFA_DELLE
 ID TNFA_DELLE STANDARD: PRT; 233 AA.
 AC O8WNR1:
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
 DE ligand superfamily member 2) (Cachectin).
 DE TNF OR TNFSF2 OR TNFA.
 GN Delphinapterus leucas (Beluga whale).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;
 OC Monodontidae; Delphinapterus.
 OX NCBI_TaxID=9749;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA PubMed=11768130;
 RA Denis F., Archambault D.;
 RT "Molecular cloning and characterization of beluga whale
 RT (Delphinapterus leucas) interleukin-1beta and tumor necrosis
 RT factor-alpha".
 RT Can. J. Vet. Res. 65:233-240(2001).
 RL
 CC -I- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
 CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
 CC induce cell death of certain tumor cell lines. It is potent
 CC pyrogen causing fever by direct action or by stimulation of
 CC interleukin 1 secretion and is implicated in the induction of
 CC cachexia, under certain conditions it can stimulate cell
 CC proliferation and induce cell differentiation (By similarity).
 CC -I- SUBUNIT: Homotrimer (By similarity).
 CC -I- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
 CC extracellular soluble form (By similarity).
 CC -I- PTM: The soluble form derives from the membrane form by
 CC proteolytic processing (By similarity).
 CC -I- PTM: The membrane form, but not the soluble form, is
 CC phosphorylated on serine residues. Dephosphorylation of the
 CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
 CC similarity).
 CC -I- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AF320323; AAL56946.1; -.
 CC InterPro: IPR003636; TNF_abc.
 CC InterPro: IPR000478; TNF_family.
 CC Pfam: PF00229; TNF; 1.
 CC PRINTS: PR01234; TNECROSISFCT.
 CC PRODOM: PD002012; TNF_abc; 1.
 CC SMART: SM00207; TNF; 1.
 CC PROSITE: PS00251; TNF_1; 1.
 CC PROSITE: PS50049; TNF_2; 1.
 CC DR Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Phosphorylation;
 CC KW signal-anchor.
 CC FT CHAIN 1 233
 CC FT CHAIN 1 233
 CC FT DOMAIN 1 35
 CC FT TRANSMEM 36 56
 CC FT SIGNAL-ANCHOR (POTENTIAL).
 CC FT CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 36 56
 CC FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 CC FT DOMAIN 57 233
 CC FT SITE 76 78
 CC FT MOD_RES 2 2
 CC FT DISULFID 145 177
 CC FT CARBOHYD 95 95
 CC FT N-LINKED (GLCNAC...) (POTENTIAL).
 CC SO SEQUENCE 233 AA; 25420 MW; 2DF37DCB2BC9E961 CRC64;
 CC
 CC Query Match 93.3%; Score 83; DB 1; Length 233;
 CC Best Local Similarity 87.5%; Pred. No. 5.5e-07;

Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YSOVLFKGGCPSRV 16
 |||||:|||||:
 Db 135 YSOVLFKGGCPSRV 150

RESULT 9

TNFA_FELCA STANDARD; PRT; 233 AA.

AC P19101;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
 ligand superfamily member 2) (Cachectin).
 GN TNF OR TNFSF2 OR TNFA.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=91016860; PubMed=2216740;
 RA McGraw R.A., Coffee B.W., Otto C.M., Drews R.T., Rawlings C.A.;
 RT "Gene sequence of feline tumor necrosis factor alpha";
 RL Nucleic Acids Res. 18:5563-5563(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Bone marrow;
 RA Daniel S.L., Brenner C.A., Legendre A.M., Solomon A., Rouse B.T.;
 RL Submitted (XXX-1993) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: cytokine that binds to TNFRSF1A/TNFR1 and
 TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
 induce cell death of certain tumor cell lines. It is potent
 pyrogen causing fever by direct action or by stimulation of
 interleukin 1 secretion and is implicated in the induction of
 cachexia, under certain conditions it can stimulate cell
 proliferation and induce cell differentiation.
 CC -1- SUBUNIT: Homotrimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
 extracellular soluble form (By similarity).
 CC -1- PTM: The soluble form derives from the membrane form by
 proteolytic processing (By similarity).
 CC -1- PTM: The membrane form, but not the soluble form, is
 phosphorylated on serine residues. Dephosphorylation of the
 membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
 similarity).
 CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
 CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
 AND MALNUTRITION.
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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 CC -----
 CC EMBL: X54000; CA37948.1; -;
 CC EMBL: M92061; AAA30818.1; -;
 CC DR HSP: S11688; S11688.
 CC DR HSP: P01375; 4TSV.
 CC DR InterPro: IPR003636; TNF_family.
 CC DR InterPro: IPR000478; TNF_family.
 CC Pfam: PF00229; TNF_1.
 CC PRINTS: PR01234; TNECRSISFCT.
 CC PRODOM: PD002012; TNF_abcd; 1.
 CC SMART: SM00207; TNF_1.
 CC PROSITE: PS00251; TNF_1; 1.

DR PROSITE: PS50049; TNF_2; 1.
 KM Cytokine; Cytotoxin; Transmembrane; Phosphorylation; Signal-anchor.
 FT CHAIN 1 233 TUMOR NECROSIS FACTOR, MEMBRANE FORM.
 FT CHAIN 77 233 TUMOR NECROSIS FACTOR, SOLUBLE FORM.
 FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT DOMAIN 57 233 EXTRACELLULAR (POTENTIAL).
 FT SITE 76 77 CLEAVAGE (BY ADAM17) (BY SIMILARITY).
 FT MOD_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
 FT DISULFID 145 177 BY SIMILARITY.
 FT CONFLICT 28 28 G -> R (IN REF. 2).
 FT CONFLICT 104 104 R -> W (IN REF. 2).
 FT CONFLICT 151 151 L -> H (IN REF. 2).
 FT CONFLICT 155 155 A -> T (IN REF. 2).
 FT CONFLICT 210 210 T -> A (IN REF. 2).
 SQ SEQUENCE 233 AA; 25322 MW; 4340239567862506 CRC64;

Query Match 93.3%; Score 83; DB 1; Length 233;
 Best local Similarity 93.8%; Pred. No. 5; 5e-07;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 YSOVLFKGGCPSRV 16
 |||||:|||||:
 Db 135 YSOVLFKGGCPSRV 150

RESULT 10

TNFA_TURTR STANDARD; PRT; 233 AA.

AC Q9BEA1;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
 ligand superfamily member 2) (Cachectin).
 GN TNF OR TNFSF2 OR TNFA.
 OS Turrisops truncatus (Atlantic bottlenose dolphin).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
 OC Turrisops.
 OX NCBI_TaxID=9739;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=11587733;
 RA Shoji Y., Inoue Y., Sugisawa H., Ito T., Endo T., Sakai T.;
 RT "Molecular cloning and functional characterization of bottlenose
 RT dolphin (Turrisops truncatus) tumor necrosis factor alpha";
 RL Vet. Immunol. Immunopathol. 82:183-192(2001).
 CC -1- FUNCTION: cytokine that binds to TNFRSF1A/TNFR1 and
 TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
 induce cell death of certain tumor cell lines. It is potent
 pyrogen causing fever by direct action or by stimulation of
 interleukin 1 secretion and is implicated in the induction of
 cachexia, under certain conditions it can stimulate cell
 proliferation and induce cell differentiation (By similarity).
 CC -1- SUBUNIT: Homotrimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
 extracellular soluble form (By similarity).
 CC -1- PTM: The soluble form derives from the membrane form by
 proteolytic processing (By similarity).
 CC -1- PTM: The membrane form, but not the soluble form, is
 phosphorylated on serine residues. Dephosphorylation of the
 membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
 similarity).
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
 CC -----
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CC or send an email to license@isb-sib.ch).
CC EMBL: AB049358; BAB39855.1; -.
DR HSSP: P01375; 4TSV.
DR InterPro: IPR003636; TNF_abc.
DR InterPro: IPR000478; TNF_family.
DR Pfam: PF00229; TNF_1.
DR PRINTS: PR01234; TNECROSISFCT.
DR ProDom: PD002012; TNF_abc; 1.
DR SMART: SM00207; TNF_1.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS50049; TNF_2; 1.
KW Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Phosphorylation;
KW Signal-anchor.
FT CHAIN 1 233 TUMOR NECROSIS FACTOR, MEMBRANE FORM.
FT DOMAIN 78 233 TUMOR NECROSIS FACTOR, SOLUBLE FORM.
FT TRANSMEM 1 35 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 57 233 EXTRACELLULAR (POTENTIAL).
FT SITE 77 78 CLEAVAGE (BY ADAM17) (BY SIMILARITY).
FT MOD_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
FT DISULFID 145 177 BY SIMILARITY.
FT CARBOHYD 95 95 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 233 AA; 25404 MW; 71CC39C699C49D9 CRC64;

Query Match 93.3%; Score 83; DB 1; Length 233;
Best Local Similarity 87.5%; Pred. No. 5.5e-07;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 YSOVLFGGCGCPSTHV 16
Db 135 YSOVLFGGCGCPSTHL 150

RESULT 11
TNFA_PIG STANDARD: PRT; 232 AA.
AC P23563;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
ligand superfamily member 2) (Cachectin).
GN TNF OR TNFSF2 OR TNFA.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9623;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91016861; Pubmed=2216741;
RA Drews R.T., Coffee B.W., Prestwood A.K., McGraw R.A.;
RT "Gene sequence of porcine tumor necrosis factor alpha.";
RL Nucleic Acids Res. 18:5564-5564(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Liver;
RA MEDLINE=91340150; Pubmed=1874444;
RA Kuhnert P., Wuehrich C., Peterhans E., Pauli U.;
RT "The porcine tumor necrosis factor encoding genes: sequence and
RT comparative analysis.";
RL Gene 102:171-178(1991).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Macrophage;
RA Choi C.S., Molitor T.W., Lin G.F., Murtough M.P.;
RT "Complete nucleotide sequence of a cDNA encoding porcine tumor
RL necrosis factor-alpha.";
RL Anim. Biotechnol. 2:97-105(1991).
RN [4]
RP SEQUENCE FROM N.A.
RP STRAIT=large white; TISSUE=Fibroblast;

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RX MEDLINE=21108615; Pubmed=11169259;
RA Chardon P., Rogel-Gaillard C., Cattolico L., Duprat S., Vainan M.,
RA Renard C.;
RT "Sequence of the swine major histocompatibility complex region
RT containing all non-classical class I genes.";
RL Tissue Antigens 57:55-65(2001).
RN [5]
RP SEQUENCE OF 44-232 FROM N.A.
RX MEDLINE=90034181; Pubmed=2478420;
RA Pauli U., Beutler B., Peterhans E.;
RT "Porcine tumor necrosis factor alpha: cloning with the polymerase
RT chain reaction and determination of the nucleotide sequence.";
RL Gene 81:185-191(1989).
CC -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
CC induce cell death of certain tumor cell lines. It is potent
CC pyrogen causing fever by direct action or by stimulation of
CC interleukin 1 secretion and is implicated in the induction of
CC cachexia. Under certain conditions it can stimulate cell
CC proliferation and induce cell differentiation.
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- EXTRACELLULAR LOCATION: Type II membrane protein. Also exists as an
CC extracellular soluble form (By similarity).
CC -!- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -!- PTM: The membrane form, but not the soluble form, is
CC phosphorylated on serine residues. Dephosphorylation of the
CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC similarity).
CC -!- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC AND MAINTENITION.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC -----
DR EMBL: X54001; CAA37949.1; -.
DR EMBL: X54859; CAA38639.1; -.
DR EMBL: X57321; CAA40591.1; -.
DR EMBL: AJ251914; CAB63852.1; -.
DR EMBL: M29079; AAA31128.1; -.
DR PIR: S12606; S12606.
DR PIR: S17290; S17290.
DR PIR: S18965; S18965.
DR HSSP: P01375; 4TSV.
DR InterPro: IPR003636; TNF_abc.
DR InterPro: IPR000478; TNF_family.
DR Pfam: PF00229; TNF_1.
DR PRINTS: PR01234; TNECROSISFCT.
DR ProDom: PD002012; TNF_abc; 1.
DR SMART: SM00207; TNF_1.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS50049; TNF_2; 1.
KW Cytokine; Cytotoxin; Transmembrane; Phosphorylation; Signal-anchor.
FT CHAIN 1 232 TUMOR NECROSIS FACTOR, MEMBRANE FORM.
FT CHAIN 77 232 TUMOR NECROSIS FACTOR, SOLUBLE FORM.
FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 57 232 EXTRACELLULAR (POTENTIAL).
FT SITE 76 77 CLEAVAGE (BY ADAM17) (BY SIMILARITY).
FT MOD_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
FT DISULFID 144 176 BY SIMILARITY.
SQ SEQUENCE 232 AA; 25254 MW; 65B28F702D99C8BE CRC64;

Query Match 88.8%; Score 79; DB 1; Length 232;
Best Local Similarity 87.5%; Pred. No. 2.6e-06;

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Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 YSOVLFKGGCPSFHV 16
 |||||:|||||:
 Db 134 YSOVLFKGGCPSFHV 149

RESULT 12

TNFA_BOVIN
 ID TNFA_BOVIN STANDARD: PRT: 233 AA.
 AC Q06599; 018779;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
 ligand superfamily member 2) (Cachectin).
 GN TNF OR TNFSF2 OR TNFA.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 NCBI_TaxID=9913;
 RN NCBI
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94083525; PubMed=8260599;
 RA Cludts I., Cleuter Y., Kettmann R., Bury A., Droogmans L.;
 RT "Cloning and characterization of the tandemly arranged bovine
 RT lymphotoxin and tumour necrosis factor-alpha genes.";
 RL Cytokine 5:336-341(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Boran, and N'Dama;
 RA Iragi F.;
 RT "Bovine TNF-alpha gene.";
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 50-233 FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=96006582; PubMed=7590981;
 RA Mertens B.E.L.C., Murtiku M., Gaidulis L.;
 RT "Cloning of two members of the TNF-superfamily in cattle: CD40 ligand
 RT and tumor necrosis factor alpha.";
 RL Immunogenetics 42:430-431(1995).
 CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
 CC TNFRSF1B/TNFR2. It is mainly secreted by macrophages and can
 CC induce cell death of certain tumor cell lines. It is potent
 CC pyrogen causing fever by direct action or by stimulation of
 CC interleukin 1 secretion and is implicated in the induction of
 CC cachexia. Under certain conditions it can stimulate cell
 CC proliferation and induce cell differentiation.
 CC -1- SUBUNIT: Homotrimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
 CC extracellular soluble form (By similarity).
 CC -1- PTM: The soluble form derives from the membrane form by
 CC proteolytic processing (By similarity).
 CC -1- PTM: The membrane form, but not the soluble form, is
 CC phosphorylated on serine residues. Dephosphorylation of the
 CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
 CC similarity).
 CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
 CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
 CC AND MALNUTRITION.
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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 CC -----
 CC EMBL: Z14137; CAA78511.1; -

DR EMBL: AF011926; AAB84086.1; -
 DR EMBL: AF011927; AAB84087.1; -
 DR EMBL: Z48808; CAA88743.1; -
 DR PIR: S24642; S24642.
 DR HSSP: P01375; 4TSV.
 DR InterPro: IPR003636; TNF_abc.
 DR InterPro: IPR00478; TNF_family.
 DR Pfam: PF00229; TNF; 1.
 DR PRINTS: PR01234; TNCRSISRCT.
 DR ProDom: PD02012; TNF_abc; 1.
 DR SMART: SM00207; TNF; 1.
 DR PROSITE: PS00251; TNF_1; 1.
 DR PROSITE: PS0049; TNF 2; 1.
 KW Cytokine; Cytotoxin; Transmembrane; Phosphorylation; Signal-anchor;
 KW Polymorphism.
 FT CHAIN 1 233 TUMOR NECROSIS FACTOR, MEMBRANE FORM.
 FT CHAIN 78 233 TUMOR NECROSIS FACTOR, SOLUBLE FORM.
 FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT DOMAIN 57 233 EXTRACELLULAR (POTENTIAL).
 FT SITE 77 78 CLEAVAGE (BY ADAM17) (BY SIMILARITY).
 FT MOD_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
 FT DISULFID 145 177 BY SIMILARITY.
 FT VARIANT 48 48 F -> C (IN STRAIN N'DAMA).
 FT CONFLICT 62 62 E -> EQ (IN REF. 3).
 SO SEQUENCE 233 AA; 25439 MW; 8AF5C002A9763B0 CRC64;

Query Match 83.1%; Score 74; DB 1; Length 233;
 Best Local Similarity 92.9%; Pred. No. 1.9e-05;
 Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YSOVLFKGGCPSFHV 14
 |||||:|||||:
 Db 135 YSOVLFKGGCPSFHV 148

RESULT 13

TNFA_MARMO
 ID TNFA_MARMO STANDARD: PRT: 233 AA.
 AC Q35734;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
 ligand superfamily member 2) (Cachectin).
 GN TNF OR TNFSF2 OR TNFA.
 OS Marmota monax (Woodchuck).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Scluridae; Sclurinae;
 OC Marmota.
 NCBI_TaxID=9995;
 RN NCBI
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98139533; PubMed=9472070;
 RA Lohrengel B., Lu M., Rogendorf M.;
 RT "Molecular cloning of the woodchuck cytokines: TNF-alpha, IFN-gamma,
 RT and IL-6.";
 RL Immunogenetics 47:332-335(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Peripheral blood;
 RA Zhou H., Hu J., Seeger C.;
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20184748; PubMed=10721723;
 RA Li D.H., Haveli E.A., Brown C.L., Cullen J.M.;
 RT "Woodchuck lymphotoxin-alpha, -beta and tumor necrosis factor genes:
 RT structure, characterization and biological activity.";
 RL Gene 242:295-305(2000).

CC -i- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
 CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
 CC induce cell death of certain tumor cell lines. It is potent
 CC pyrogen causing fever by direct action or by stimulation of
 CC interleukin 1 secretion and is implicated in the induction of
 CC cachexia, under certain conditions it can stimulate cell
 CC proliferation and induce cell differentiation.
 CC -i- SUBUNIT: Homotrimer (By similarity).
 CC -i- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
 CC extracellular soluble form (By similarity).
 CC -i- PTM: The soluble form derives from the membrane form by
 CC proteolytic processing (By similarity).
 CC -i- PTM: The membrane form, but not the soluble form, is
 CC phosphorylated on serine residues. Dephosphorylation of the
 CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
 CC similarity).
 CC -i- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
 CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
 CC AND MALNUTRITION.
 CC -i- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: Y14137; CAA74569.1; -
 CC EMBL: AF082491; AAC32615.1; -
 CC EMBL: AF012910; AAF34863.1; -
 CC HSSP: P06804; 2TNF.
 CC InterPro: IPR003636; TNF_ab.
 CC InterPro: IPR000478; TNF_family.
 CC Pfam: PF00229; TNF_1.
 CC PRINTS: PR01234; TNCRSISFCT.
 CC PRODOM: PD002012; TNF_ab.
 CC SMART: SM00207; TNF_1.
 CC PROSITE: PS00251; TNF_1; 1.
 CC PROSITE: PS50049; TNF_2; 1.
 CC KMW Cytokine; Cytotoxin; Transmembrane; Phosphorylation; Signal-anchor.
 CC FT CHAIN 1 233 TUMOR NECROSIS FACTOR, MEMBRANE FORM.
 CC FT CHAIN 78 233 TUMOR NECROSIS FACTOR, SOLUBLE FORM.
 CC FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 CC (POTENTIAL).
 CC FT DOMAIN 57 233 EXTRACELLULAR (POTENTIAL).
 CC FT SITE 77 78 CLEAVAGE (BY ADAM17) (BY SIMILARITY).
 CC FT MOD_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
 CC FT DISULFID 146 177 BY SIMILARITY.
 CC SQ SEQUENCE 233 AA; 25764 MW; 34BDD1965DAAE07 CRC64;

Query Match Score 73; DB 1; Length 233;
 Best local Similarity 78.9%; Pred. No. 2.8e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 YSOVLFKGGCCPS---TH 15
 Db 136 YSOVLFKGGCCPSYVLLTH 154

RESULT 14
 TNFA_CAVPO STANDARD; PRT; 234 AA.
 AC PS1435;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
 DE ligand superfamily member 2) (Cachectin).
 GN TNF OR TNFSF2 OR TNFA.
 OS Cavia porcellus (Guinea pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia.
 OX NCBI_TaxID:10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Hartley; TISSUE-Lung;
 RA Yuan H.T., Kelly F.J., Bingle C.D.;
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Dunkin-Hartley;
 RA MEDLINE-97462215; PubMed-9316485;
 RX White A.M., Yoshimura T., Smith A.W., Westwick J., Watson M.L.;
 RT "Airway inflammation induced by recombinant guinea pig tumor necrosis
 RT factor-alpha";
 RL Am. J. Physiol. 273:L524-L530(1997).
 CC -i- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
 CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
 CC induce cell death of certain tumor cell lines. It is potent
 CC pyrogen causing fever by direct action or by stimulation of
 CC interleukin 1 secretion and is implicated in the induction of
 CC cachexia, under certain conditions it can stimulate cell
 CC proliferation and induce cell differentiation.
 CC -i- SUBUNIT: Homotrimer (By similarity).
 CC -i- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
 CC extracellular soluble form (By similarity).
 CC -i- PTM: The soluble form derives from the membrane form by
 CC proteolytic processing (By similarity).
 CC -i- PTM: The membrane form, but not the soluble form, is
 CC phosphorylated on serine residues. Dephosphorylation of the
 CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
 CC similarity).
 CC -i- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
 CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
 CC AND MALNUTRITION.
 CC -i- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: U39839; AAB06492.1; -
 CC EMBL: U77036; AAB19210.1; -
 CC HSSP: P06804; 2TNF.
 CC InterPro: IPR003636; TNF_ab.
 CC InterPro: IPR000478; TNF_family.
 CC Pfam: PF00229; TNF_1.
 CC PRINTS: PR01234; TNCRSISFCT.
 CC PRODOM: PD002012; TNF_ab.
 CC SMART: SM00207; TNF_1.
 CC PROSITE: PS00251; TNF_1; 1.
 CC PROSITE: PS50049; TNF_2; 1.
 CC KMW Cytokine; Cytotoxin; Transmembrane; Phosphorylation; Signal-anchor.
 CC FT CHAIN 1 234 TUMOR NECROSIS FACTOR, MEMBRANE FORM.
 CC FT CHAIN 80 234 TUMOR NECROSIS FACTOR, SOLUBLE FORM.
 CC FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 CC (POTENTIAL).
 CC FT DOMAIN 57 234 EXTRACELLULAR (POTENTIAL).
 CC FT SITE 79 80 CLEAVAGE (BY ADAM17) (BY SIMILARITY).
 CC FT MOD_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
 CC FT DISULFID 147 178 BY SIMILARITY.
 CC SQ SEQUENCE 234 AA; 25793 MW; 7272C940393E7E9B CRC64;

Query Match Score 73; DB 1; Length 234;
 Best local Similarity 78.9%; Pred. No. 2.8e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 YSOVLFKGGCCPS---TH 15

Db 137 YSOVLFGGCGCPSTLLTH 155

```

RESULT 15
TNEA_CAPHI STANDARD; PRT; 234 AA.
ID TNEA_CAPHI STANDARD; PRT; 234 AA.
AC P13296; 028320; 09MY22;
DT 01-JUN-1990 (Rel. 13, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
GN ligand superfamily member 2) (Cachectin).
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleenocyte;
RA Takakura H., Mori Y., Tatsumi M.;
RT "Molecular cloning of caprine TNF-alpha cDNA and its expression in
RT E.coli and insect cells."
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 41-234 FROM N.A.
RA Goldstein I.M., Henner D., Talhouk A.;
RL Submitted (MAR-1989) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 44-234 FROM N.A.
RC TISSUE=Ovarian follicle;
RA Wang B., Zhang Y.;
RT "Goat ovarian TNF alpha cDNA sequence."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 75-234 FROM N.A.
RC TISSUE=Blood;
RA Rimsstad E.;
RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC TNFRSF1B/TNFR2. It is mainly secreted by macrophages and can
CC induce cell death of certain tumor cell lines. It is potent
CC pyrogen causing fever by direct action or by stimulation of
CC interleukin 1 secretion and is implicated in the induction of
CC cachexia, under certain conditions it can stimulate cell
CC proliferation and induce cell differentiation.
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC extracellular soluble form (By similarity).
CC -1- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -1- PTM: The membrane form, but not the soluble form, is
CC phosphorylated on serine residues. Deposphorylation of the
CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC similarity).
CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC AND MALNUTRITION.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -1- CAUTION: Ref.2 sequence differs from that shown due to a
CC frameshift in position 60.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D86587; BAA13130.1; -.

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DR EMBL; X14828; CAA32937.1; ALT_FRAME.
DR EMBL; AE276985; AAF87741.1; -.
DR EMBL; X77317; CAA54523.1; -.
DR PIR; S06192; S06192.
DR HSSP; P01375; 4TSV.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
KW Cytokine; Cytotoxicity; Transmembrane; Phosphorylation; Signal-anchor.
FT CHAIN 1 234
FT DOMAIN 1 35
FT TRANSMEM 36 56
FT DOMAIN 57 233
FT MOD_RES 2 2
FT SITE 78 79
FT DISULFID 146 178
FT CARBOHYD 96 96
FT CONFLICT 79 79
FT CONFLICT 119 119
FT CONFLICT 129 129
FT CONFLICT 155 155
FT CONFLICT 164 164
FT CONFLICT 184 184
FT CONFLICT 185 185
FT CONFLICT 215 215
SQ SEQUENCE 234 AA; 25519 MW; 976BE33BBAB041 CRC64;
Query Match 77.5%; Score 69; DB 1; Length 234;
Best Local Similarity 85.7%; Pred. No. 0.00014;
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

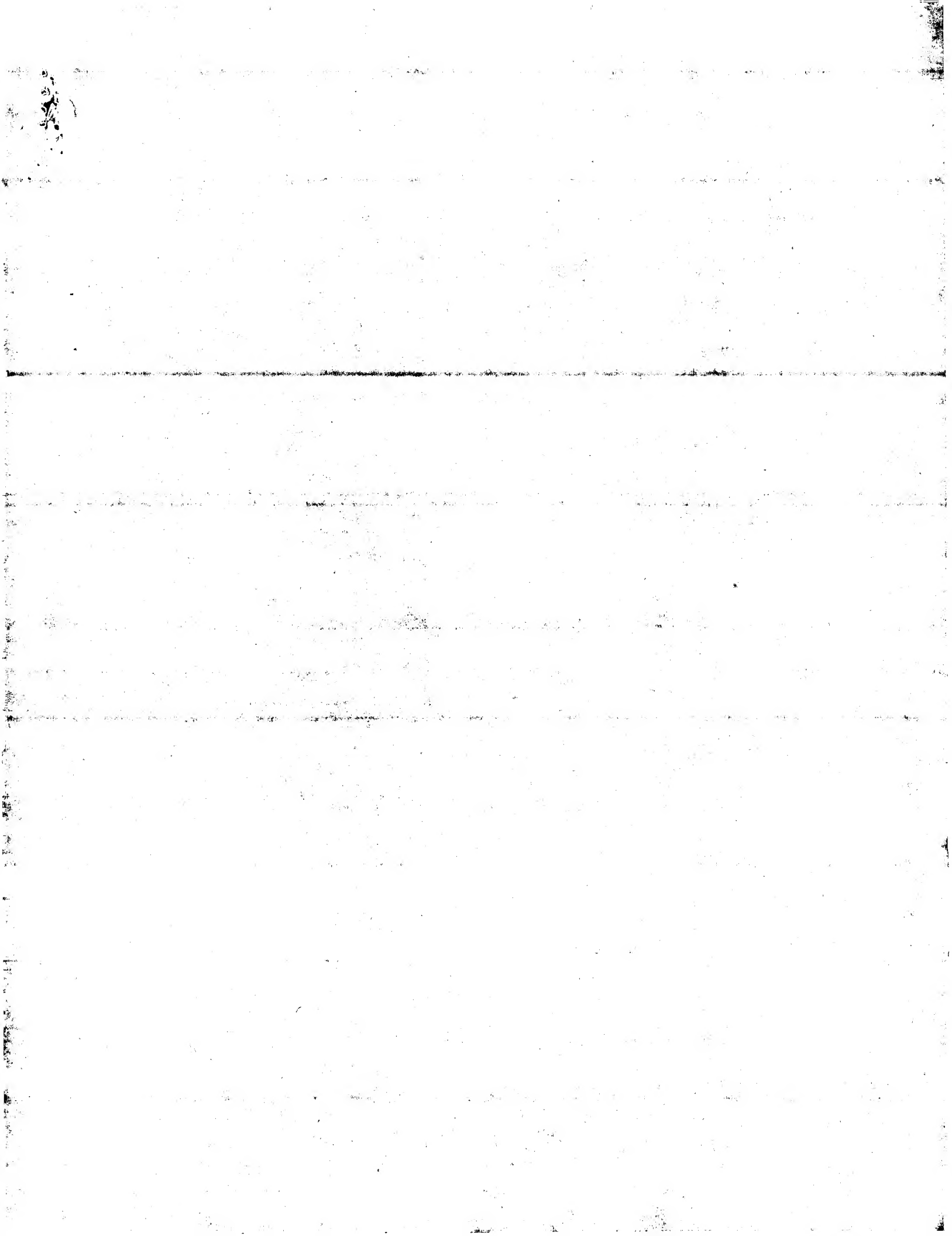
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Search completed: December 4, 2002, 13:23:01
Job time : 7.31579 secs

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QY 1 YSOVLFGGCGCPST 14
Db 136 YSOVLFGGCGCPST 149

```



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 4, 2002, 13:20:58 ; Search time 21.0526 Seconds
(without alignments)
156.596 Million cell updates/sec

Title: US-09-754-004-1

Perfect score: 89

Sequence: 1 YSQVLFKGGCPSTHV 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriap.*
17: sp_archaea.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	89	100.0	99	6 Q95LE8	Q95LE8 canis famil
2	89	100.0	149	6 Q97543	Q97543 aotus nancy
3	89	100.0	157	4 Q43647	Q43647 homo sapien
4	89	100.0	215	6 Q9BEE8	Q9BEE8 erinaceus e
5	89	100.0	232	4 Q9UIV3	Q9UIV3 homo sapien
6	89	100.0	234	6 Q9TTJ3	Q9TTJ3 equus cabal
7	84	94.4	217	6 Q9BEG0	Q9BEG0 cyclopes di
8	79	88.8	217	6 Q9BEG1	Q9BEG1 bradyopus tr
9	78	87.6	65	6 Q95N81	Q95N81 canis famil
10	77	86.5	138	6 Q9TTG7	Q9TTG7 aotus lemur
11	77	86.5	149	6 Q97538	Q97538 aotus vocif
12	77	86.5	149	6 Q9TTG8	Q9TTG8 aotus nigri
13	77	86.5	217	6 Q9BEF4	Q9BEF4 cabassous u
14	74	83.1	104	6 Q27978	Q27978 bos taurus
15	73	82.0	216	6 Q9BEC4	Q9BEC4 talpa europ
16	70	78.7	216	11 Q70332	Q70332 mesocricetu

17	69	77.5	235	11 Q9JI27	Q9JI27 rattus norv
18	69	77.5	235	11 Q9JI26	Q9JI26 rattus norv
19	68	76.4	101	11 Q9RI36	Q9RI36 meriones pr
20	67	75.3	216	6 Q9BEC9	Q9BEC9 ochotona pr
21	65	73.0	215	11 Q99ND1	Q99ND1 tamiasciuru
22	64	71.9	217	6 Q9BEC5	Q9BEC5 tenrec ecau
23	62	69.7	217	11 Q9BERG6	Q9BERG6 peromyscus
24	50.5	56.7	214	6 Q9BEF3	Q9BEF3 didelphis m
25	48.5	54.5	216	6 Q9BEE0	Q9BEE0 macropus ru
26	47	52.8	521	4 Q9C016	Q9C016 homo sapien
27	47	52.8	604	4 Q96M94	Q96M94 homo sapien
28	46	51.7	361	2 Q93G67	Q93G67 escherichia
29	45	50.6	156	11 Q91ZL4	Q91ZL4 sigmodon hi
30	44.5	50.0	169	11 Q9WV90	Q9WV90 marmota mon
31	44	49.4	218	11 Q9D9F9	Q9D9F9 mus musculu
32	44	49.4	257	11 Q91WE8	Q91WE8 mus musculu
33	44	49.4	491	16 Q97HA7	Q97HA7 clostridium
34	43	48.3	93	6 Q9TTJ2	Q9TTJ2 bos taurus
35	43	48.3	111	11 Q91ZF6	Q91ZF6 mesocricetu
36	43	48.3	615	10 Q8S4R4	Q8S4R4 lycopersico
37	42	47.2	290	5 Q9VC76	Q9VC76 drosophila
38	42	47.2	372	16 Q9K3H2	Q9K3H2 streptomyce
39	42	47.2	776	5 Q8SRL6	Q8SRL6 encephalito
40	41.5	46.6	319	16 Q8ZJ39	Q8ZJ39 yersinia pe
41	41	46.1	91	5 Q968U5	Q968U5 ascogregari
42	41	46.1	91	5 Q968U4	Q968U4 ascogregari
43	41	46.1	91	5 Q968U3	Q968U3 ascogregari
44	41	46.1	141	13 Q9DG78	Q9DG78 ictalurus p
45	41	46.1	280	10 Q8RV01	Q8RV01 oryza sativ

ALIGNMENTS

RESULT 1

Q95LE8 PRELIMINARY; PRT; 99 AA.
AC Q95LE8;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE TNF-alpha (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BLOOD;
RA Chamizo C., Rubio J.M., Moreno J., Alvar J.;
RT "Semi-quantification of canine cytokine expression by one tube RT-PCR.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF327899; AAL26919.1; .
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRODOM; PD002012; TNF_abc; 1.
DR PROSITE; PS00251; TNF_1; UNKNOWN_1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER 1
FT NON_TER 99
SQ SEQUENCE 99 AA; 10760 MW; 3977AE499F00D7B0 CRC64;

Query Match 100.0%; Score 89; DB 6; Length 99;

Best Local Similarity 100.0%; Pred. No. 5.1e-08;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSQVLFKGGCPSTHV 16

Db 60 YSQVLFKGGCPSTHV 75

RESULT 2

ID O97543 PRELIMINARY; PRT; 149 AA.
AC O97543;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
DE Tumor necrosis factor alpha (Fragment).
GN TNF-ALPHA.
OS Aotus nancymae (Owl monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=37293;
RN [1]
RP SEQUENCE FROM N.A.
RA Echeverry S.J., Hernandez E., Moreno A., Patarroyo M.E., Murillo L.A.;
RT "Identification, cloning and sequencing of different interleukin genes
in 4 Aotus species.";
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF014513; AAD01539.1; -.
DR HSSP; P01375; 4TSV.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER 1
FT NON_TER 149
SQ SEQUENCE 149 AA; 16466 MW; 3C2A6140778EFA8A CRC64;

Query Match 100.0%; Score 89; DB 6; Length 149;

Best Local Similarity 100.0%; Pred. No. 7.5e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSOVLFGGCGCPSTHV 16
|||||
Db 52 YSOVLFGGCGCPSTHV 67

RESULT 3

O43647
ID O43647 PRELIMINARY; PRT; 157 AA.
AC O43647;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Tumor necrosis factor alpha (Fragment).
GN TNFA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Jang J.S., Kim B.E.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF043342; AAC03542.1; -.
DR HSSP; P01375; IABM.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER 1
SQ SEQUENCE 157 AA; 17380 MW; D1344822267B9F20 CRC64;

Query Match 100.0%; Score 89; DB 4; Length 157;

Best Local Similarity 100.0%; Pred. No. 7.9e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSOVLFGGCGCPSTHV 16
|||||
Db 59 YSOVLFGGCGCPSTHV 74

RESULT 4

O9BEE8
ID O9BEE8 PRELIMINARY; PRT; 215 AA.
AC O9BEE8;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Tumor necrosis factor (Fragment).
GN TNFA.
OS Erinaceus europaeus (Western European hedgehog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceinae; Erinaceus.
OX NCBI_TaxID=9365;
RN [1]
RP SEQUENCE FROM N.A.
RA van Dijk M.A.M., de Jong W.W.;
RT "Indels indicate that rodents are monophyletic and lagomorphs are
their sister group.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ286830; CAC28522.1; -.
DR HSSP; P01375; 4TSV.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER 1
FT NON_TER 215
SQ SEQUENCE 215 AA; 23696 MW; 3E337E7E65F074EA CRC64;

Query Match 100.0%; Score 89; DB 6; Length 215;

Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSOVLFGGCGCPSTHV 16
|||||
Db 125 YSOVLFGGCGCPSTHV 140

RESULT 5

O9UIV3
ID O9UIV3 PRELIMINARY; PRT; 232 AA.
AC O9UIV3;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Tumor necrosis factor.
GN TNF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93272029; PubMed=8499947;
RA Iris F., Bouqueleret L., Prieur S., Caterina D., Primas G., Perrot V.,
RA Jurka J., Rodriguez-Tome P., Claverie J., Cohen D., Dausset J.;
RT "Dense Alu clustering and a potential new member of the NFKappaB
family within a 90 kilobase HLA class III segment.";
RL Nac. Genet. 3:137-145(1993).
RN [2]
RP SEQUENCE FROM N.A.

RA MEDLINE-96215741; PubMed-8629302;
RA Utans U., Quist W.C., McManus B.M., Wilson J.E., Arceci R.J.,
RA Wallace A.F., Russell M.E.;
RT "Allograft inflammatory factor-1. A cytokine-responsive macrophage
RT molecule expressed in transplanted human hearts.";
RL Transplantation 61:1387-1392(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE-96006565; PubMed-7509964;
RX Holzinger I., de Baey A., Messer G., Kick G., Zwierzina H.,
RA Weiss E.H.;
RT "Cloning and genomic characterization of LST1: a new gene in the human
RT TNF region.";
RL Immunogenetics 42:315-322(1995).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE-93208881; PubMed-7916655;
RX Browning J.L., Ngam-ek A., Lawton P., DeMarinis J., Tizard R.,
RA Chow E.P., Hession C., O'Brine-Greco B., Foley S.F., Ware C.F.;
RT "Lymphotoxin-beta: A new member of the TNF family that forms a
RT heteromeric complex with lymphotoxin on the cell surface.";
RL Cell 72:847-856(1993).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE-86016093; PubMed-2995927;
RX Nedwin G.E., Naylor S.L., Sakaguchi A.Y., Smith D., Jarrett-Nedwin J.,
RA Pennica D., Goeddel D.V., Gray P.W.;
RT "Human lymphotoxin and tumor necrosis factor genes: structure,
RT homology and chromosomal localization.";
RL Nucleic Acids Res. 13:6361-6373(1985).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE-91086846; PubMed-1670638;
RX Messer G., Spengler U., Jung M.C., Honold G., Bloemer K., Pape G.R.,
RA Rietmueller G., Weiss E.H.;
RT "Polymorphic Structure of the Tumor Necrosis Factor (TNF) Locus: An
RT Ncol Polymorphism in the First Intron of the Human TNF-beta Gene
RT Correlates with A Variant Amino Acid in Position 26 and a Reduced
RT Level of TNF-beta Production.";
RL J. Exp. Med. 173:209-219(1991).
RN [7]
RP SEQUENCE FROM N.A.
RX MEDLINE-91139175; PubMed-1671667;
RX Abraham L.J., Du D.C., Zahedi K., Dawkins R.L., Whitehead A.S.;
RT "Haplotypic polymorphisms of the TNFB gene.";
RL Immunogenetics 33:50-53(1991).
RN [8]
RP SEQUENCE FROM N.A.
RX MEDLINE-94362679; PubMed-8081366;
RX Albertella M.R., Campbell D.R.;
RT "Characterization of a novel gene in the human major
RT histocompatibility complex that encodes a potential new member of the
RT I kappa B family of proteins.";
RL Hum. Mol. Genet. 3:793-799(1994).
RN [9]
RP SEQUENCE FROM N.A.
RX MEDLINE-95324911; PubMed-7601445;
RX Peelman L., Chardon P., Nunes M., Renard C., Geffroy C., Vaiman M.,
RA Van Zeveren A., Coppieters W., Van de Weghe A., Bouquet Y., Choy W.,
RA Strominger J., Spies T.;
RT "The BAT1 Gene in the MHC Encodes an Evolutionarily Conserved Putative
RT Nuclear RNA Helicase of the D-E-A-D Family.";
RL Genomics 26:210-218(1995).
RN [10]
RP SEQUENCE FROM N.A.
RX MEDLINE-20132445; PubMed-10668961;
RX Neville M.J., Campbell R.D.;
RT "Alternative splicing of the LST-1 gene located in the major
RT histocompatibility complex on human chromosome 6.";
RL DNA Seq. 8:155-160(1997).
RN [11]
RP SEQUENCE FROM N.A.
RX MEDLINE-98035883; PubMed-9367684;

de Baey A., Fellerhoff B., Maier S., Martinozzi S., Weidle U.,
RA Weiss E.H.;
RT "Complex expression pattern of the TNF region gene LST1 through
RT differential regulation, initiation, and alternative splicing.";
RL Genomics 45:591-600(1997).
RN [12]
RP SEQUENCE FROM N.A.
RX MEDLINE-98149985; PubMed-9480751;
RX Shilina T., Tamiya G., Oka A., Yamagata T., Yamagata N., Kikkawa E.,
RA Goto K., Mizuki N., Watanabe K., Fukuzumi Y., Taguchi S., Sugawara C.,
RA Ono A., Chen L., Yamazaki M., Tashiro H., Ando A., Ikemura T.,
RA Kimura M., Inoko H.;
RT "Nucleotide sequencing analysis of the 146-kilobase segment around the
RT IKBL and MICA genes at the centromeric end of the HLA class I
RT region.";
RL Genomics 47:372-382(1998).
DR EMBL: Y14768; CAA5070.1; -.
DR HSSP: P01375; 4TSV.
DR InterPro: IPR003636; TNF_abc.
DR InterPro: IPR000478; TNF_family.
DR Pfam: PF00229; TNF; 1.
DR PRINTS: PR01234; TNECROSISFCT.
DR ProDom: PD002012; TNF_abc; 1.
DR SMART: SM00207; TNF; 1.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS50049; TNF_2; 1.
SQ SEQUENCE 232 AA; 25446 MW; E4D71B19C6AE0D03 CRC64;
Query Match 100.0%; Score 89; DB 4; Length 232;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YSQVLFKGGCPSSTHV 16
Db 134 YSQVLFKGGCPSSTHV 149
RESULT 6
Q9TTJ3 PRELIMINARY; PRT; 234 AA.
AC Q9TTJ3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Tumor necrosis factor-alpha.
GN TNFA.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=THOROUGHRED; TISSUE=ARTERIAL ENDOTHELIUM;
RA Ishida N., Sato F., Hasegawa T.;
RT "Molecular cloning of equine tumor necrosis factor-alpha mRNA.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: A8035735; BAA88349.1; -.
DR HSSP: P01375; 1A8W.
DR InterPro: IPR003636; TNF_abc.
DR InterPro: IPR000478; TNF_family.
DR Pfam: PF00229; TNF; 1.
DR PRINTS: PR01234; TNECROSISFCT.
DR ProDom: PD002012; TNF_abc; 1.
DR SMART: SM00207; TNF; 1.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS50049; TNF_2; 1.
SQ SEQUENCE 234 AA; 25430 MW; 2384D4950A21F377 CRC64;
Query Match 100.0%; Score 89; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YSQVLFKGGCPSSTHV 16

Db 136 YSQVLFKGGCGCPSTHV 151
|||||

RESULT 7

Q9BEG0 PRELIMINARY; PRT; 217 AA.
AC Q9BEG0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Tumor necrosis factor (Fragment).
GN TNFA.
OS Cyclopes didactylus (silky anteater).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Edentata; Myrmecophagidae; Cyclopes.
OX NCBI_TaxID=84074;
RN [1]
RP SEQUENCE FROM N.A.
RA van Dijk M.A.M., de Jong W.W.;
RT "Indels indicate that rodents are monophyletic and lagomorphs are their sister group."
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ286828; CAC28513.1; -
DR HSSP; P01375; IABM.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD02012; TNF_abc; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER 1
FT NON_TER 217
SQ SEQUENCE 217 AA; 23753 MW; F760E887F6C29EBB CRC64;

Query Match 94.4%; Score 84; DB 6; Length 217;
Best Local Similarity 93.8%; Pred. No. 8.2e-07;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSQVLFKGGCGCPSTHV 16
|||||

Db 127 YSQVLFKGGCGCPSTHV 142

RESULT 8

Q9BEG1 PRELIMINARY; PRT; 217 AA.
AC Q9BEG1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Tumor necrosis factor (Fragment).
GN TNFA.
OS Bradypus tridactylus (Pale-throated three-toed sloth).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Edentata; Bradypodidae; Bradypus.
OX NCBI_TaxID=9354;
RN [1]
RP SEQUENCE FROM N.A.
RA van Dijk M.A.M., de Jong W.W.;
RT "Indels indicate that rodents are monophyletic and lagomorphs are their sister group."
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ286827; CAC28513.1; -
DR HSSP; P01375; IABM.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD02012; TNF_abc; 1.
DR SMART; SM00207; TNF; 1.

DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER 1
FT NON_TER 217
SQ SEQUENCE 217 AA; 23655 MW; A7056710B6238074 CRC64;
Query Match 88.8%; Score 79; DB 6; Length 217;
Best Local Similarity 93.8%; Pred. No. 6.2e-06;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSQVLFKGGCGCPSTHV 16
|||||

Db 127 YSQVLFKGGCGCPSTHV 142

RESULT 9

Q95N81 PRELIMINARY; PRT; 65 AA.
ID Q95N81;
AC Q95N81;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Tumor necrosis factor alpha (fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Fonfara S., Groene A., Koenig M., Wolfgang B.;
RT "Sequence of canine tumor necrosis factor alpha mRNA in DH82-cells."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF349537; AAK54071.1; -
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD02012; TNF_abc; 1.
DR PROSITE; PS00251; TNF_1; UNKNOWN_1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER 1
FT NON_TER 65
SQ SEQUENCE 65 AA; 7065 MW; 917C467A05F42B5B CRC64;

Query Match 87.6%; Score 78; DB 6; Length 65;
Best Local Similarity 93.8%; Pred. No. 2.9e-06;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSQVLFKGGCGCPSTHV 16
|||||

Db 28 YSQVLFKGGCGCPSTHV 43

RESULT 10

Q9TTG7 PRELIMINARY; PRT; 138 AA.
ID Q9TTG7;
AC Q9TTG7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Tumor necrosis factor alpha (fragment).
GN TNF-ALPHA.
OS Aotus lemurinus (Northern gray-necked night monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=43147;
RN [1]
RP SEQUENCE FROM N.A.
RA Murillo L.A., Hernandez E., Echeverry S.J., Mendez J.A.,
RA Patarro M.E.;
RT "Aotus lemurinus gene for TNF alpha."
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF097329; AAF21304.1; -
DR HSSP; P01375; 4TSV.

DR InterPro: IPR003636; TNF_abc.
DR InterPro: IPR000478; TNF_family.
DR Pfam: PF00229; TNF; 1.
DR PRINTS: PR01234; TNECROSISFCT.
DR ProDom: PD002012; TNF_abc; 1.
DR SMART: SM00207; TNF; 1.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS00049; TNF_2; 1.
FT NON_TER 1
SQ SEQUENCE 138 AA; 15269 MW; 29275EE4F4CD5068 CRC64;

Query Match 86.5%; Score 77; DB 6; Length 138;
Best Local Similarity 100.0%; Pred. No. 8.9e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSQVLFKGGGCPST 14
|||||

Db 52 YSQVLFKGGGCPST 65

RESULT 11
O97538

ID O97538 PRELIMINARY; PRT; 149 AA.

AC O97538;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Tumor necrosis factor alpha (Fragment).
GN TNF-ALPHA.

OS Aotus vociferans (noisy night monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=57176;
RN [1]

RP SEQUENCE FROM N.A.

RA Echeverry S.J., Hernandez E., Moreno A., Patarroyo M.E., Murillo L.A.;
RT "Identification, cloning and sequencing of different interleukin genes
in 4 Aotus species.";
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF014508; AAD01534.1; -.

DR HSSP: P01375; 4TSV.

DR InterPro: IPR003636; TNF_abc.

DR Pfam: PF00229; TNF; 1.

DR PRINTS: PR01234; TNECROSISFCT.

DR ProDom: PD002012; TNF_abc; 1.

DR SMART: SM00207; TNF; 1.

DR PROSITE: PS00251; TNF_1; 1.

DR PROSITE: PS00049; TNF_2; 1.

FT NON_TER 1

FT NON_TER 149

SQ SEQUENCE 149 AA; 16415 MW; 86F1B9BCED16E689 CRC64;

Query Match 86.5%; Score 77; DB 6; Length 149;
Best Local Similarity 100.0%; Pred. No. 9.6e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSQVLFKGGGCPST 14
|||||

Db 52 YSQVLFKGGGCPST 65

RESULT 12
Q9TTG8

ID Q9TTG8 PRELIMINARY; PRT; 149 AA.

AC Q9TTG8;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Tumor necrosis factor alpha (Fragment).

GN TNF-ALPHA.

OS Aotus nigriceps (black-headed night monkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=57175;
RN [1]
RP SEQUENCE FROM N.A.
RA Murillo L.A., Hernandez E., Echeverry S.J., Mendez J.A.,
RA Patarroyo M.E.;
RT "Aotus nigriceps gene for TNF alpha.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF097328; AAF21303.1; -.
DR HSSP: P01375; 4TSV
DR InterPro: IPR003636; TNF_abc.
DR InterPro: IPR000478; TNF_family.
DR Pfam: PF00229; TNF; 1.
DR PRINTS: PR01234; TNECROSISFCT.
DR ProDom: PD002012; TNF_abc; 1.
DR SMART: SM00207; TNF; 1.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS00049; TNF_2; 1.
FT NON_TER 1
FT NON_TER 149

SQ SEQUENCE 149 AA; 16415 MW; 86F1B9BCED16E689 CRC64;

Query Match 86.5%; Score 77; DB 6; Length 149;
Best Local Similarity 100.0%; Pred. No. 9.6e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSQVLFKGGGCPST 14
|||||

Db 52 YSQVLFKGGGCPST 65

RESULT 13
Q9BEF4

ID Q9BEF4 PRELIMINARY; PRT; 217 AA.

AC Q9BEF4;

DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Tumor necrosis factor (Fragment).

GN TNFA.

OS Cabassous unicinctus (Southern naked-tailed armadillo).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Edentata; Dasypodidae; Cabassous.

OX NCBI_TaxID=48852;

RN [1]

RP SEQUENCE FROM N.A.

RA van Dijk M.A.M., de Jong W.W.;

RT "Indels indicate that rodents are monophyletic and lagomorphs are
their sister group.";

RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AJ286829; CAC28518.1; -.

DR HSSP: P01375; 4TSV.

DR InterPro: IPR003636; TNF_abc.

DR InterPro: IPR000478; TNF_family.

DR Pfam: PF00229; TNF; 1.

DR PRINTS: PR01234; TNECROSISFCT.

DR ProDom: PD002012; TNF_abc; 1.

DR SMART: SM00207; TNF; 1.

DR PROSITE: PS00251; TNF_1; 1.

DR PROSITE: PS00049; TNF_2; 1.

FT NON_TER 1

FT NON_TER 217

SQ SEQUENCE 217 AA; 23742 MW; 83C591DD6883FD86 CRC64;

Query Match 86.5%; Score 77; DB 6; Length 217;
Best Local Similarity 87.5%; Pred. No. 1.4e-05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YSQVLFKGGGCPSTHV 16
|||||

Db 127 YSQVLFKGGGCPSTHV 142

```
RESULT 14
Q27978 PRELIMINARY; PRT; 104 AA.
AC Q27978;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE TNFA (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HOLSTEIN;
RA Dietz A.B., Neibergs H.L., Kehrli M.E.;
RT "Development of a Bovine TNFA Single Strand Conformational
RT Polymorphism.";
RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U11040; AAA19573.1; -.
DR HSSP; P01375; 4TSV.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER 1
FT NON_TER 104
FT NON_TER 104 104
SQ SEQUENCE 104 AA; 11662 MW; BCR0A76D9FFA44BD CRC64;

Query Match 83.1%; Score 74; DB 6; Length 104;
Best Local Similarity 92.9%; Pred. No. 2.3e-05;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSQVLFGQGCPST 14
Db 46 YSQVLFGQGCPST 59
|||||:|||||

RESULT 15
Q9BEC4 PRELIMINARY; PRT; 216 AA.
AC Q9BEC4;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Tumor necrosis factor (Fragment).
GN TNFA.
OS Talpa europaea (European mole).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Insectivora; Talpidae; Talpa.
OX NCBI_TaxID=9375;
RN [1]
RP SEQUENCE FROM N.A.
RA van Dijk M.A.M., de Jong W.W.;
RT "Indels indicate that rodents are monophyletic and lagomorphs are
RT their sister group.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ286831; CAC28539.1; -.
DR HSSP; P01375; 1A8M.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER 1
FT NON_TER 104 104
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FT NON_TER 216
SQ SEQUENCE 216 AA; 23542 MW; FFEFE8DBBD27836 CRC64;

Query Match 82.0%; Score 73; DB 6; Length 216;
Best Local Similarity 87.5%; Pred. No. 6.9e-05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YSQVLFGQGCPSTHV 16
Db 126 YSQVLFGQGCPSTNLY 141
|||||:|||||
|||||:|||||

Search completed: December 4, 2002, 13:23:59
Job time : 22.0526 secs
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GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: December 4, 2002, 13:18:13 ; Search time 26.1053 seconds
(without alignments)
81.670 Million cell updates/sec

Title: US-09-754-004-1

Perfect score: 89

Sequence: 1 YSQLFKGCGCPSTHW 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
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- 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	89	100.0	22	18 AAW22949	htNF-alpha epitope
2	89	100.0	22	19 AAW59148	Human tumour necro
3	89	100.0	140	16 AAR72456	Tumour necrosis fa
4	89	100.0	145	9 AAP82043	Sequence of new tu
5	89	100.0	147	9 AAP81853	Sequence of modifi
6	89	100.0	147	22 AAB67245	Human tumour necro
7	89	100.0	147	22 AAP71982	C-terminal region
8	89	100.0	149	10 AAP91635	Polypeptide derive
9	89	100.0	149	11 AAR05612	Antitumour peptide
10	89	100.0	150	8 AAP70528	Synthetic tumour n

11	89	100.0	150	8 AAP71245	TNF-derived polype
12	89	100.0	150	9 AAP81236	Modified tumour ne
13	89	100.0	150	9 AAP82190	TNF analogue: AA
14	89	100.0	150	9 AAP82303	TNF analogue: AA
15	89	100.0	150	9 AAP81086	Sequence of new ph
16	89	100.0	150	9 AAP81068	Sequence of new ph
17	89	100.0	150	10 AAP91906	Tumoricidal polype
18	89	100.0	150	10 AAP95660	Anti-tumour active
19	89	100.0	150	11 AAR05286	New polypeptide wi
20	89	100.0	150	11 AAR08151	Polypeptide with a
21	89	100.0	150	12 AAR11011	TNF-like polypepti
22	89	100.0	150	12 AAR11723	Tumour Necrosis Fa
23	89	100.0	150	13 AAR29808	TNF analogue #1.
24	89	100.0	150	13 AAR29809	TNF analogue #2.
25	89	100.0	150	13 AAR22311	TNF polypeptide mu
26	89	100.0	150	15 AAR69584	Human TNF mutein.
27	89	100.0	150	15 AAR69579	Human TNF mutein.
28	89	100.0	150	15 AAR69580	Human TNF mutein.
29	89	100.0	150	15 AAR69581	Human TNF mutein.
30	89	100.0	150	15 AAR69582	Human TNF mutein.
31	89	100.0	150	15 AAR69583	Human TNF mutein.
32	89	100.0	151	9 AAP81231	Tumoricidal polypep
33	89	100.0	151	9 AAP81233	Anti-tumour peptid
34	89	100.0	151	9 AAP81231	Sequence of modifi
35	89	100.0	151	10 AAP93187	Polypeptide with a
36	89	100.0	151	11 AAR05865	Anti-tumour peptid
37	89	100.0	151	11 AAR07900	Antitumour polypep
38	89	100.0	151	12 AAR11615	Tumour Necrosis Fa
39	89	100.0	151	12 AAR11613	Tumour Necrosis Fa
40	89	100.0	151	12 AAR11714	Tumour necrosis fa
41	89	100.0	151	12 AAR11860	Truncated Tumour N
42	89	100.0	151	12 AAR11861	Improved Tumour Ne
43	89	100.0	151	12 AAR11753	Tumour Necrosis Fa
44	89	100.0	151	12 AAR11667	Human TNF with mod
45	89	100.0	151	12 AAR11968	Tumour Necrosis Fa

ALIGNMENTS

RESULT 1

AAW22949

ID AAW22949 standard; peptide; 22 AA.

XX

AC AAW22949;

XX

DT 05-MAR-1998 (first entry)

XX

DE htNF-alpha epitope 59-80.

XX

KW tumour necrosis factor alpha; TNF; epitope; antibody; antagonist;

KW fibrinogen; cardiovascular; cerebrovascular; thrombosis; stroke;

KW thrombophlebitis; myocardial infarction; embolism; ischaemia.

XX

OS Homo sapiens.

XX

PN WO9730088-A2.

XX

PD 21-AUG-1997.

XX

PF 17-FEB-1997; 97WO-GB00435.

XX

PR 16-FEB-1996; 96US-0602272.

XX

XX (KENN-) KENNEDY INST RHEUMATOLOGY.

XX Elliott MJH, Feldmann M, Maini RN;

XX WPI; 1997-424980/39.

DR

XX Treating and preventing cardiovascular, cerebrovascular or

PT thrombotic disorder, or decreasing plasma fibrinogen - by

PT administration of tumour necrosis factor antagonist

XX PS Claim 10; Page 14; 57pp; English.

XX CC The invention relates to the use of an antagonist of tumour necrosis

XX CC factor (TNF) for the treatment of vascular disease, cardiovascular

XX CC disorders, thrombotic disorders, or illnesses or pathologies which

XX CC are treatable by decreasing plasma fibrinogen. Typical conditions which

XX CC can be treated include acute myocardial infarction, deep vein thrombosis,

XX CC thrombophlebitis, stroke, thromboembolic disorder or ischemic events.

XX CC In one embodiment the antagonist used is an anti-TNF antibody

XX CC (optionally chimeric, humanised or resurfaced), preferably one which

XX CC binds to an epitope comprising at least 5 amino acids within the region

XX CC TNF-alpha 87-108 and/or TNF-alpha 59-80. The present sequence represents

XX CC the 59-80 epitope.

XX SQ Sequence 22 AA;

Query Match 100.0%; Score 89; DB 18; Length 22;

Best Local Similarity 100.0%; Pred. No. 1.1e-06;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSQVLFKGGGCPSTHV 16

Db 1 YSQVLFKGGGCPSTHV 16

|||||

RESULT 2

AAW59148

ID AAW59148 standard; peptide; 22 AA.

XX AC AAW59148;

XX DT 13-AUG-1998 (first entry)

XX DE Human tumour necrosis factor-alpha epitope pos. 59-80.

XX KW Tumour necrosis factor-alpha; epitope; human immunodeficiency virus;

XX KW HIV; TNF-alpha; anti-TNF; antibody; treatment; prevention; infection;

XX KW acquired immune deficiency disease; interleukin-2; IL-2; gene therapy;

XX KW systemic toxicity; CD4+ cell; inflammation; immune response.

XX OS Homo sapiens.

XX PN WO9811917-A1.

XX PD 26-MAR-1998.

XX PF 17-SEP-1997; 97WO-US16116.

XX PR 19-SEP-1996; 96US-0716107.

XX PA (CENZ) CENTOCOR INC.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI McCloskey RV, Walker RE, Woody JN;

XX DR WPI; 1998-230303/20.

XX PT Treating or preventing acquired immune deficiency syndrome using

XX PT interleukin-2 - and antibodies against tumour necrosis factor, to

XX PT reduce side effects of the treatment

XX PS Claim 10; Page 11; 50pp; English.

XX CC This peptide sequence is a fragment of tumour necrosis factor-alpha

XX CC (TNF-alpha) corresponding to amino acid position 59-80 of the full

XX CC length protein. This region is an epitope and is recognized and/or binds

XX CC with anti-TNF activity. This fragment is used to describe a novel method

XX CC of treating or preventing acquired immune deficiency disease and

XX CC infection with human immune deficiency virus (HIV) by co-administration

XX CC of interleukin-2 (IL-2) and a chimeric antibody (Ab), or its fragment,

XX CC against tumour necrosis factor (TNF). IL-2 and Ab are administered by

XX CC injection, orally, topically or are produced from gene therapy vectors,

CC but preferably by intravenous injection or infusion. Usual doses are

CC 0.01-100 (especially 1-40) mg/kg/day, in 1-6 portions or in sustained

CC release form. Further doses may be given, just before or during relapse.

CC Inhibition of TNF alpha by Ab alleviates some of the systemic toxicity

CC associated with administration of IL-2 (which increases the level of CD4+

CC cells but also stimulates production of TNF, high levels of which cause

CC unwanted inflammatory and immunological responses). Blockade of TNF

CC allows administration of higher doses of IL-2 than would be otherwise

XX possible.

XX SQ Sequence 22 AA;

Query Match 100.0%; Score 89; DB 19; Length 22;

Best Local Similarity 100.0%; Pred. No. 1.1e-06;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSQVLFKGGGCPSTHV 16

Db 1 YSQVLFKGGGCPSTHV 16

|||||

RESULT 3

AAR72456

ID AAR72456 standard; protein; 140 AA.

XX AC AAR72456;

XX DT 19-DEC-1995 (first entry)

XX DE Tumour necrosis factor-alpha 4th exon fragment.

XX KW Tumour necrosis factor; fusion protein; metastasis; inhibition.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Misc-difference 1

FT /note= "This residue has the peptide AAR72454

FT attached at the N-terminus"

XX PN TW239078-A.

XX PD 21-JAN-1995.

XX PF 12-OCT-1993; 93TW-0108498.

XX PR 29-SEP-1993; 93JP-0020556.

XX PA (MIZU/) MIZUNO D.

XX PA (SONA/) SONAMOTO I.

XX PI Sonamoto I;

XX DR WPI; 1995-168947/22.

XX PT Pharmaceutical and veterinary composition for inhibiting metastasis

XX PT - can be made into tablet form

XX PS Disclosure; Page 5; 14pp; Chinese.

XX CC The amino acid sequence of a part of the 4th exon from the tumour

XX CC necrosis factor (TNF)-alpha. The protein has the peptide AAR72454

XX CC attached to the N-terminal amino acid. The fusion protein can be

XX CC used in pharmaceutical compositions for inhibiting metastasis.

XX SQ Sequence 140 AA;

Query Match 100.0%; Score 89; DB 16; Length 140;

Best Local Similarity 100.0%; Pred. No. 6.4e-06;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSQVLFKGGGCPSTHV 16

|||||

Db 42 YSQVLFKGGCPSTHV 57

RESULT 4
AAP82043
ID AAP82043 standard; protein; 145 AA.
XX
XX AAP82043;
AC
XX 12-DEC-1990 (first entry)
DT
XX Sequence of new tumour necrosis factor (TNF).
DE
XX Anticancer drug; lymphokine; antitumour.
KW
XX Homo sapiens.
OS
XX JP63032486-A.
PN
XX 12-FEB-1988.
PD
XX 25-JUL-1986; 86JP-0173822.
PF
XX 25-JUL-1986; 86JP-0173822.
PR
XX (TEIJ) TEIJIN KK.
PA
XX WPI; 1988-080331/12.
DR
XX New biologically active polypeptide - useful as anticancer agent
PT
XX Claim 2(1); Page 547; 17pp; Japanese.
PS
XX New biologically active polypeptide has cytotoxic activity specifically
CC for tumour cells and, therefore, is expected to be used as an anticancer
CC drug. It is derived from human TNF by deleting 11 N-terminal AAs. (See
CC also J63188396, AAN81624 and AAP81236).
CC
XX
XX Sequence 145 AA;
SQ

Query Match 100.0%; Score 89; DB 9; Length 145;
Best Local Similarity 100.0%; Pred. No. 6.6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSQVLFKGGCPSTHV 16
|||||
Db 48 YSQVLFKGGCPSTHV 63

RESULT 5
AAP81853
ID AAP81853 standard; protein; 147 AA.
XX
XX AAP81853;
AC
XX 17-DEC-1990 (first entry)
DT
XX Sequence of modified human tumour necrosis factor (hTNF).
DE
XX Antitumour; anticancer; cytostatic.
KW
XX Homo sapiens.
OS
XX JP62272991-A.
PN
XX 27-NOV-1987.
PD
XX 21-MAY-1986; 86JP-0114754.
PF
XX 21-MAY-1986; 86JP-0114754.
PR
XX (TEIJ) TEIJIN KK.
PA
XX
XX

Query Match 100.0%; Score 89; DB 22; Length 147;
Best Local Similarity 100.0%; Pred. No. 6.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSQVLFKGGCPSTHV 16
|||||
Db 49 YSQVLFKGGCPSTHV 64

RESULT 6
AAB67245
ID AAB67245 standard; protein; 147 AA.
XX
XX AAB67245;
AC
XX 18-APR-2001 (first entry)
DT
XX Human tumour necrosis factor alpha.
DE
XX Human; Apo2 ligand; divalent metal ions; viral infection; cancer.
KW
XX Homo sapiens.
OS
XX WO200100832-A1.
PN
XX 04-JAN-2001.
PD
XX 26-JUN-2000; 2000WO-US17579.
PF
XX 28-JUN-1999; 99US-0141342.
PR
XX (GETH) GENENTECH INC.
PA
XX Ashkenazi AJ, Hymowitz S, Kelley RF, Koumenis I, Leung S;
PI O'Connell M, Pai R, Shahrokh Z, Simmons L;
XX
XX WPI; 2001-123012/13.
DR
XX Use of divalent metal ions for making Apo-2 ligand and in formulations
PT containing Apo-2 ligand for increasing yield and stability of ligand
PT trimers, useful for therapeutic applications -
XX
XX Disclosure; Fig 3; 60pp; English.
XX
XX The present invention relates to a formulation comprising Apo-2
CC ligand and divalent metal ions. Apo-2 ligand and the formulation
CC are useful for treating cancers and viral infections. Addition
CC of divalent metal ions for making Apo-2 ligand and formulations
CC containing Apo-2 ligand results in increased yield and stability
CC of Apo-2 ligand trimers.
XX
XX Sequence 147 AA;
SQ

Query Match 100.0%; Score 89; DB 9; Length 147;
Best Local Similarity 100.0%; Pred. No. 6.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSQVLFKGGCPSTHV 16
|||||
Db 49 YSQVLFKGGCPSTHV 64

DR WPI; 1988-010365/02.
XX N-PSDB; AAN82306.
XX New bioactive polypeptide -
PT has antitumour activity, and is obtd. by culturing bacteria
PT transformed with plasmid contg. DNA sequence of the polypeptide
XX
XX Claim 2(1); Page 761; 20pp; Japanese.
PS
XX DNA sequence encoding hTNF was synthesised chemically and inserted into
CC vector plasmid. Recombinant plasmid was cut with restriction enzyme and
CC DNA fragment coding for new bioactive polypeptide was obtd. The new
CC bioactive polypeptide has ten N-terminal AAs deleted. It has antitumour
CC activity greater than hTNF and can be produced by culturing bacteria
CC transformed with a plasmid contg. DNA encoding the polypeptide.
XX
XX Sequence 147 AA;
SQ

Query Match 100.0%; Score 89; DB 9; Length 147;
Best Local Similarity 100.0%; Pred. No. 6.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSQVLFKGGCPSTHV 16
|||||
Db 49 YSQVLFKGGCPSTHV 64

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSQVLFGGQCPSTHV 16
 |||||
 Db 49 YSQVLFGGQCPSTHV 64

RESULT 7

AA71982
 ID AAY71982 standard; Protein; 147 AA.

XX AAY71982;

XX AAY71982;

XX 28-MAR-2001 (first entry)

XX C-terminal region of human Tumour Necrosis Factor (TNF).

KW Human; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;
 KW Tumour necrosis factor and Apol-related Leucocyte expressed Ligand 1;
 KW therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis;
 KW systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;
 KW thrombocytopenia purpura; acute rheumatic fever; myasthenia gravis;
 KW haemolytic anaemia; Grave's disease; Goodpasture's syndrome;
 KW post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA;
 KW B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH Region 2..8
 FT /label= Beta_strand
 FT Region 16..18
 FT /label= Beta_strand
 FT Region 26..28
 FT /label= Beta_strand
 FT Region 31..34
 FT /label= Beta_strand
 FT Region 37..40
 FT /label= Beta_strand
 FT Region 45..56
 FT /label= Beta_strand
 FT Region 66..71
 FT /label= Beta_strand
 FT Region 80..90
 FT /label= Beta_strand
 FT Region 104..114
 FT /label= Beta_strand
 FT Region 119..127
 FT /label= Beta_strand
 FT Region 140..147
 FT /label= Beta_strand

XX WO200068378-A1.

XX 16-NOV-2000.

XX 05-MAY-2000; 2000WO-US12266.

XX 06-MAY-1999; 99US-0132892.

XX 01-MAY-2000; 2000US-0201012.

XX (NAJE-) NAT JEWISH MEDICAL & RES CENT.

XX Shu HS;

XX WPI; 2001-016094/02.

XX Isolated TALL-1 protein is used to identify compounds that regulate B
 PT lymphocyte proliferation, used to treat B lymphocyte associated
 PT autoimmune disorders

XX Example 1; Fig 1b; 112pp; English.

XX

CC The present invention relates to Tumour necrosis factor (TNF) and
 CC Apol-related Leucocyte expressed Ligand 1 (TALL-1) nucleic acid
 CC molecules, proteins (including homologues), and their antibodies. The
 CC invention in particular relates to methods for regulating the
 CC interaction between TALL-1 and TALL-1 receptors (BCMA referred as B cell
 CC maturation factor) to regulate monocyte, macrophage and B lymphocyte
 CC mediated immune responses. TALL-1 protein is useful for identifying
 CC compounds that regulate B lymphocyte proliferation. It is also useful for
 CC treating B lymphocyte associated autoimmune disorders like rheumatoid
 CC arthritis, systemic lupus erythematosus (SLE), insulin dependent diabetes
 CC mellitus, multiple sclerosis, myasthenia gravis, Grave's disease,
 CC autoimmune haemolytic anaemia, autoimmune thrombocytopenia purpura,
 CC Goodpasture's syndrome, pemphigus vulgaris, acute rheumatic fever,
 CC post-streptococcal glomerulonephritis, or polyarteritis nodosa.
 CC The TALL-1 protein and its corresponding nucleic acid sequence are also
 CC useful in diagnostic assays.
 CC The present sequence is a C-terminal region of human Tumour necrosis
 CC factor (TNF) which has 20-25% sequence identity with C-terminal region of
 CC human TALL-1 protein extracellular domain.

XX Sequence 147 AA;

Query Match 100.0%; Score 89; DB 22; Length 147;

Best Local Similarity 100.0%; Pred. No. 6.7e-06;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSQVLFGGQCPSTHV 16

|||||

Db 49 YSQVLFGGQCPSTHV 64

RESULT 8

AA71982

ID AAP91635 standard; protein; 149 AA.

XX AAP91635;

XX 25-JUN-1990 (first entry)

XX Polypeptide derived from human tumour necrosis factor.

XX Tumour necrosis factor; antitumour activity; pTNF482.

XX Homo sapiens.

XX JP01023898-A.

XX 26-JAN-1989.

XX 17-JUL-1987; 87JP-0177284.

XX 17-JUL-1987; 87JP-0177284.

XX (TEIJ) TEIJIN KK.

XX WPI; 1989-072158/10.

XX N-PSDB; AAN94432.

XX New physiologically active polypeptide - with antitumour activity.

XX Claim 1; page 1; 18pp; Japanese.

XX The recombinant polypeptide expressed by E.coli transformed with pTNF482,
 CC has antitumour activity with greater specific activity and stability than
 CC natural h-TNF, and which causes less side effects.

XX Sequence 149 AA;

Query Match 100.0%; Score 89; DB 10; Length 149;

Best Local Similarity 100.0%; Pred. No. 6.8e-06;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSQVLFGGQCPSTHV 16

Db 51 YSQVLFKGGCPSTHV 66
|||||

RESULT 9

AAR05612
ID AAR05612 standard; protein; 149 AA.

XX AC AAR05612;

XX DT 29-OCT-1990 (first entry)

XX DE Antitumour peptide.

XX KW Antitumour; cancer; tumour necrosis factor; ds.

XX OS Synthetic.

XX PN JP02128696-A.

XX PD 17-MAY-1990.

XX PE 09-NOV-1988; 88JP-0281364.

XX PR 09-NOV-1988; 88JP-0281364.

XX PA (TEIJ) TEIJIN KK.

XX DR WPI; 1990-196692/26.

XX DR N-PSDB; AAQ05038.

XX PT New physiologically active polypeptide -

XX PT contains specific amino acid sequence, shows antitumour effect

XX PT and has low side effect.

XX PS Disclosure; ; 18pp; Japanese.

XX CC DNA is synthesised from 17 oligonucleotides TNF-1 to TNF-17.

XX CC The gene product may be truncated by 12 N-terminal AAs, and

XX CC residue Leu-157 may be replaced by Phe

XX SQ Sequence 149 AA;

Query Match 100.0%; Score 89; DB 11; Length 149;

Best Local Similarity 100.0%; Pred. No. 6.8e-06;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSQVLFKGGCPSTHV 16

Db 52 YSQVLFKGGCPSTHV 67
|||||

RESULT 10

AAP70528
ID AAP70528 standard; protein; 150 AA.

XX AC AAP70528;

XX DT 30-JAN-1991 (first entry)

XX DE Synthetic tumour necrosis factor mutant.

XX KW Tumour necrosis factor; mutant; antitumour agent; vector pTNF 416;

XX PN JP62248498-A.

XX PD 29-OCT-1987.

XX PF 21-APR-1986; 86JP-0090087.

XX PR 21-APR-1986; 86JP-0090087.

XX PA (TEIJ) TEIJIN KK.

XX DR WPI; 1987-345004/49.

XX DR N-PSDB; AAN70852.

XX PT New bioactive polypeptide - having antitumour activity and higher

XX PT activity than human tumour necrosis factor.

XX PS Claim 1; page 623; 18pp; Japanese.

XX CC The mutant of tumour necrosis factor (TNF) is constructed by

XX CC modifying the sequence of human TNF and deleting 7 N-terminal amino

XX CC acids. The mutant has activity 2.8 times that of human TNF.

XX CC It is expressed using expression vector pTNF 416 in E.coli.

XX CC The cells are then cultured to give the mutant in an amt. of 15.5%

XX CC of total proteins. The antitumour activity of this protein was

XX CC measured using mouse L-929 fibroblast cells. 100 microlitres of

XX CC E.coli lysate contg. 0.00006 units had specific activity of the

XX SQ Sequence 150 AA;

Query Match 100.0%; Score 89; DB 8; Length 150;

Best Local Similarity 100.0%; Pred. No. 6.8e-06;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSQVLFKGGCPSTHV 16

Db 52 YSQVLFKGGCPSTHV 67
|||||

RESULT 11

AAP71245
ID AAP71245 standard; Protein; 150 AA.

XX AC AAP71245;

XX DT 29-APR-1991 (first entry)

XX DE TNF-derived polypeptide.

XX KW Tumour necrosis factor.

XX OS Homo sapiens.

XX PN JP62091198-A.

XX PD 25-APR-1987.

XX PF 26-FEB-1986; 86JP-0040733.

XX PR 21-JUN-1985; 85JP-0136280.

XX PR 26-FEB-1985; 85EP-0102093.

XX PR 23-APR-1985; 85JP-0087297.

XX PR 26-FEB-1986; 86JP-0040733.

XX PA (DAIN) DAINIPPON PHARM KK.

XX DR WPI; 1987-153959/22.

XX DR N-PSDB; AAN71245.

XX PT Tumoricidal polypeptide(s) - are prepd. by cleaving specified DNA

XX PT with pertinent restriction enzyme(s) and bonding with

XX PT conventional synthetic DNA adaptor.

XX PS Claim 1; Page 1; 20pp; Japanese.

XX CC The polypeptide was obt'd. by cleaving DNA encoding mature TNF. The

XX CC resulting fragment was then ligated to a synthetic DNA adapter and

XX CC inserted into an expression vector for prodn. of the polypeptide

XX CC which has tumoricidal activity. The N-terminal may have up to three

XX CC residues deleted resulting in N-terminals of: Met-Ser-Asp-Lys,

XX CC Met-Asp-Lys, or Met-Lys.

SQ Sequence 150 AA;

Query Match 100.0%; Score 89; DB 8; Length 150;
Best Local Similarity 100.0%; Pred. No. 6.8e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSQVLFKGGGCPSTHV 16
|||||
DB 52 YSQVLFKGGGCPSTHV 67

RESULT 12

AAP81236
ID AAP81236 standard; protein; 150 AA.

AC AAP81236;

DT 15-OCR-1990 (first entry)

DE Modified tumour necrosis factor.

KW Tumour necrosis factor; cytotoxic agent; antitumour drug; cancer.

OS Synthetic.

PN JP63188396-A.

PD 03-AUG-1988.

PF 30-JAN-1987; 87JP-0018566.

PR 30-JAN-1987; 87JP-0018566.

PA (TEIJ) TEIJIN KK.

DR WPI; 1988-260396/37.

DR N-PSDB; AAN81624.

PT New biologically active polypeptide - is modified tumour necrosis factor with cytotoxic activity to cancer cells.

PS Claim 1; Page 1; 20pp; Japanese.

CC A DNA sequence produced from synthetic oligonucleotides can be used, in an expression vector, to produce the recombinant polypeptide which has a broad action spectrum and causes few side effects.

SQ Sequence 150 AA;

Query Match 100.0%; Score 89; DB 9; Length 150;
Best Local Similarity 100.0%; Pred. No. 6.8e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSQVLFKGGGCPSTHV 16
|||||
DB 52 YSQVLFKGGGCPSTHV 67

RESULT 13

AAP82190

ID AAP82190 standard; protein; 150 AA.

AC AAP82190;

DT 15-NOV-1990 (first entry)

DE TNF analogue.

KW TNF; drug compsn.

PN JP63267290-A.

PD 04-NOV-1988.

XX 23-APR-1987; 87JP-0098552.

PR 23-APR-1987; 87JP-0098552.

PA (TEIJ) TEIJIN KK.

DR WPI; 1988-357026/50.

DR N-PSDB; AAN82096.

XX New physiologically active polypeptide - is different from known human TNF protein and has antitumour activity.

PS Claim 1; Page 1; 18pp; Japanese.

CC This physiologically active peptide is produced using recombinant DNA methods and is useful as an antitumour agent. It is applied as a drug compsn. See also J63267291.

SQ Sequence 150 AA;

Query Match 100.0%; Score 89; DB 9; Length 150;

Best Local Similarity 100.0%; Pred. No. 6.8e-06;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSQVLFKGGGCPSTHV 16
|||||

DB 53 YSQVLFKGGGCPSTHV 68

RESULT 14

AAP82303

ID AAP82303 standard; protein; 150 AA.

AC AAP82303;

DT 15-NOV-1990 (first entry)

DE TNF analogue.

XX TNF; drug compsn.

PN JP63267290-A.

PD 04-NOV-1988.

XX 23-APR-1987; 87JP-0098552.

PR 23-APR-1987; 87JP-0098552.

PA (TEIJ) TEIJIN KK.

DR WPI; 1988-357026/50.

DR N-PSDB; AAN82098.

XX New physiologically active polypeptide - is different from known human TNF protein and has antitumour activity.

PS Claim 1; Page 1; 18pp; Japanese.

CC This physiologically active peptide is produced using recombinant DNA methods and is useful as an antitumour agent. It is applied as a drug compsn. See also J63267290.

SQ Sequence 150 AA;

Query Match 100.0%; Score 89; DB 9; Length 150;

Best Local Similarity 100.0%; Pred. No. 6.8e-06;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSQVLFKGGGCPSTHV 16
|||||

DB 53 YSQVLFKGGGCPSTHV 68

RESULT 15
AAP81066
ID AAP81066 standard; protein; 150 AA.
XX
XX AC AAP81066;
XX
XX DT 14-SEP-1990 (first entry)
XX
XX DE Sequence of new physiologically active polypeptide with antitumour
XX DE activity.
XX
XX KW Antitumour; Escherichia coli.
XX
XX PN JP63226298-A.
XX
XX PD 20-SEP-1988.
XX
XX PF 16-MAR-1987; 87JP-0059007.
XX
XX PR 16-MAR-1987; 87JP-0059007.
XX
XX PA (TEIJ) TEIJIN KK.
XX
XX DR WPI; 1988-305170/43.
XX DR P-PSDB; AAP81068.
XX
XX PT New physiologically active polypeptide used as antitumour agent -
XX PT obtd. by culturing recombinant Escherichia coli cell transformed by
XX PT plasmid contg. DNA region coding the polypeptide
XX
XX PS Claim 2 (4); Page 670; 20pp; Japanese.
XX
XX CC A recombinant microorganism cell transformed by recombinant plasmid
XX CC contg. the DNA region coding for the polypeptide is cultured. The
XX CC polypeptide is isolated from the resulting culture. The microorganism
XX CC is pref. Escherichia coli.
XX
SQ Sequence 150 AA;

Query Match 100.0%; Score 89; DB 9; Length 150;
Best Local Similarity 100.0%; Pred. No. 6.8e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSQVLFKKGCGCPSTHV 16
Db | | | | | | | | | | | | | | | | | |
52 YSQVLFKKGCGCPSTHV 67

Search completed: December 4, 2002, 13:22:40
Job time : 27.1053 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 4, 2002, 13:24:03 ; Search time 5.89474 Seconds
(without alignments)
44.086 Million cell updates/sec

Title: US-09-754-004-1

Perfect score: 89

Sequence: 1 YSQVLFKGGCPCSTHV 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 103943 seqs, 16242309 residues

Total number of hits satisfying chosen parameters: 103943

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description
1	89	100.0	16	US-09-754-004-1
2	89	100.0	22	US-08-602-272-1
3	89	100.0	104	US-09-911-777-5
4	89	100.0	150	US-09-877-156-25
5	89	100.0	150	US-10-116-378-28
6	89	100.0	152	US-09-779-050A-24
7	89	100.0	157	US-09-903-327A-7
8	89	100.0	157	US-09-756-301A-1
9	89	100.0	157	US-09-927-703-1
10	89	100.0	157	US-09-854-280-19
11	89	100.0	157	US-09-934-465-13
12	89	100.0	157	US-09-766-535A-1
13	89	100.0	157	US-09-854-208-19
14	89	100.0	157	US-09-756-161A-1
15	89	100.0	157	US-10-010-229-1
16	89	100.0	157	US-10-043-450-1
17	89	100.0	157	US-10-044-534-1
18	89	100.0	164	US-09-798-789-2
19	89	100.0	164	US-09-981-289-2

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20      89 100.0 193 9 US-10-145-014-3
21      89 100.0 193 10 US-09-982-308-3
22      89 100.0 233 8 US-08-971-317A-5
23      89 100.0 233 9 US-10-136-511-3
24      89 100.0 233 9 US-10-145-014-22
25      89 100.0 233 10 US-09-193-663-5
26      89 100.0 233 10 US-09-879-919-5
27      89 100.0 233 10 US-09-782-980-43
28      89 100.0 233 10 US-09-840-707A-14
29      89 100.0 233 10 US-09-246-129B-3
30      89 100.0 233 10 US-09-345-790-3
31      89 100.0 233 10 US-09-929-493-3
32      89 100.0 233 10 US-09-899-059-3
33      89 100.0 233 12 US-10-082-260-5
34      89 100.0 233 12 US-10-012-452-10
35      89 100.0 597 9 US-09-903-327A-11
36      69 77.5 151 9 US-09-779-050A-40
37      69 77.5 235 9 US-10-017-910-8
38      59 66.3 235 10 US-09-246-129B-7
39      59 66.3 235 10 US-09-899-059-7
40      59 66.3 235 12 US-10-012-452-14
41      50 56.2 102 9 US-09-779-050A-6
42      46 51.7 361 9 US-09-839-894-10
43      46 51.7 361 9 US-09-839-894-28
44      45.5 51.1 97 10 US-09-911-777-6
45      45.5 51.1 140 12 US-10-116-378-30

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ALIGNMENTS

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RESULT 1
US-09-754-004-1
; Sequence 1, Application US/09754004
; Patent No. US20020010180A1
; GENERAL INFORMATION:
; APPLICANT: Marc Feldmann
; APPLICANT: Ravinder N. Maini
; TITLE OF INVENTION: TNF Alpha Antagonists and Methotrexate
; TITLE OF INVENTION: in the Treatment of TNF-Mediated Disease
; FILE REFERENCE: 2891.1001-026
; CURRENT APPLICATION NUMBER: US/097754.004
; CURRENT FILING DATE: 2001-01-03
; PRIOR APPLICATION NUMBER: 08/690,775
; PRIOR FILING DATE: 1996-08-01
; PRIOR APPLICATION NUMBER: 08/607,419
; PRIOR FILING DATE: 1996-02-28
; PRIOR APPLICATION NUMBER: PCT/GB94/00462
; PRIOR FILING DATE: 1994-03-10
; PRIOR APPLICATION NUMBER: PCT/GB93/02070
; PRIOR FILING DATE: 1993-10-06
; PRIOR APPLICATION NUMBER: 07/958,248
; PRIOR FILING DATE: 1992-10-08
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-754-004-1

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Query Match      100.0%; Score 89; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 YSQVLFKGGCPCSTHV 16
      |||
Db      1 YSQVLFKGGCPCSTHV 16

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RESULT 2
US-08-602-272-1
; Sequence 1, Application US/08602272

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; Patent No. US20020081306A1
; GENERAL INFORMATION:
; APPLICANT: Elliott, Michael J.
; APPLICANT: Maini, Ravinder N.
; APPLICANT: Feldmann, Marc
; TITLE OF INVENTION: Methods of Preventing or Treating
; TITLE OF INVENTION: Cardiovascular, Cerebrovascular and Thrombotic Disorders
; TITLE OF INVENTION: with Tumor Necrosis Factor Antagonists
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173-4799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,272
; FILING DATE:
; CLASSIFICATION: 504
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: KIR96-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-602-272-1

Query Match 100.0%; Score 89; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.4e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSQVLFGGQGPCSTHV 16
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Db 1 YSQVLFGGQGPCSTHV 16

RESULT 3
US-09-911-777-5
; Sequence 5, Application US/09911777
; Patent No. US20020037852A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; APPLICANT: APOTEC S.A.
; APPLICANT: BROWNING, Jeffrey
; APPLICANT: AMBROSE, Christine
; APPLICANT: MACKAY, Fabienne
; APPLICANT: TSCHOPP, Jurg
; APPLICANT: SCHNEIDER, Pascal
; TITLE OF INVENTION: BAF, Inhibitors Thereof and Their Use
; TITLE OF INVENTION: in the Modulation of B-Cell Response
; FILE REFERENCE: A070 US
; CURRENT APPLICATION NUMBER: US/09/911,777
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/117,169
; PRIOR FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: 60/143,228
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: PCT/US00/01788
; PRIOR FILING DATE: 2000-01-25
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; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-911-777-5

Query Match 100.0%; Score 89; DB 10; Length 104;
Best Local Similarity 100.0%; Pred. No. 7.1e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSQVLFGGQGPCSTHV 16
| | | | | | | | | | | | | | | |
Db 34 YSQVLFGGQGPCSTHV 49

RESULT 4
US-09-877-156-25
; Sequence 25, Application US/09877156
; Patent No. US20020055625A1
; GENERAL INFORMATION:
; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/877,156
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/286,529
; PRIOR FILING DATE: 1998-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 150
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-877-156-25

Query Match 100.0%; Score 89; DB 10; Length 150;
Best Local Similarity 100.0%; Pred. No. 1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSQVLFGGQGPCSTHV 16
| | | | | | | | | | | | | | | |
Db 52 YSQVLFGGQGPCSTHV 67

RESULT 5
US-10-116-378-28
; Sequence 28, Application US/10116378
; Patent No. US20020150993A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pitti, Robert M.
; APPLICANT: Wood, William
; TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOGY AND
; TITLE OF INVENTION: NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P1206R1
; CURRENT APPLICATION NUMBER: US/10/116,378
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/247,225
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/074,087
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09
; NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 28
; LENGTH: 150
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-378-28
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Query Match 100.0%; Score 89; DB 12; Length 150;
Best Local Similarity 100.0%; Pred. No. 1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSQVLFKGGCGPSTHV 16
|||||
Db 52 YSQVLFKGGCGPSTHV 67

RESULT 6

US-09-779-050A-24
; Sequence 24, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 24
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-050A-24

Query Match 100.0%; Score 89; DB 9; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSQVLFKGGCGPSTHV 16
|||||
Db 54 YSQVLFKGGCGPSTHV 69

RESULT 7

US-09-903-327A-7
; Sequence 7, Application US/09903327A
; Patent No. US20020164333A1
; GENERAL INFORMATION:
; APPLICANT: Nemerow, Glen R.
; TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET

; FILE REFERENCE: 22908-1228
; CURRENT APPLICATION NUMBER: US/09/903,327A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 09/613,017
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Human

; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (0)...(0)
; OTHER INFORMATION: Tumor necrosis factor-alpha (TNF alpha, mature
; OTHER INFORMATION: peptide)
US-09-903-327A-7

Query Match 100.0%; Score 89; DB 9; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSQVLFKGGCGPSTHV 16

Db 59 YSQVLFKGGCGPSTHV 74
|||||

RESULT 8

US-09-756-301A-1
; Sequence 1, Application US/09756301A
; Patent No. US20010027249A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Grayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; TITLE OF INVENTION: Human Tumor Necrosis Factor
; FILE REFERENCE: 0975.1005-008
; CURRENT APPLICATION NUMBER: US/09/756,301A
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; PRIOR FILING DATE: 1991-03-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-756-301A-1

Query Match 100.0%; Score 89; DB 10; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSQVLFKGGCGPSTHV 16
|||||
Db 59 YSQVLFKGGCGPSTHV 74

RESULT 9

US-09-927-703-1
; Sequence 1, Application US/09927703
; Patent No. US20020022720A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Grayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; TITLE OF INVENTION: Human Tumor Necrosis Factor
; FILE REFERENCE: 0975.1005-013

; CURRENT APPLICATION NUMBER: US/09/927,703
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: U.S. 09/756,398
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; PRIOR FILING DATE: 1991-03-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-927-703-1

Query Match 100.0%; Score 89; DB 10; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSQVLFGKGGCPSTHV 16
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DB 59 YSQVLFGKGGCPSTHV 74

RESULT 10
US-09-854-280-19
; Sequence 19, Application US/09854280
; Patent No. US20020052027A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1C2
; CURRENT APPLICATION NUMBER: US/09/854,280
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/311,832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/085,579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 60/113,621
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 19
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-280-19

Query Match 100.0%; Score 89; DB 10; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YSQVLFGKGGCPSTHV 16
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DB 59 YSQVLFGKGGCPSTHV 74
RESULT 11
US-09-934-465-13
; Sequence 13, Application US/09934465
; Patent No. US2002010233A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: APO-2 LIGAND
; FILE REFERENCE: 11669.22US03
; CURRENT APPLICATION NUMBER: US/09/934,465
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 08/584,031
; PRIOR FILING DATE: 1996-01-09
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-934-465-13

Query Match 100.0%; Score 89; DB 10; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSQVLFGKGGCPSTHV 16
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DB 59 YSQVLFGKGGCPSTHV 74

RESULT 12
US-09-766-535A-1
; Sequence 1, Application US/09766535A
; Patent No. US20020106372A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Ghayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; FILE REFERENCE: 0975.1005-010
; CURRENT APPLICATION NUMBER: US/09/766,535A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827

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: PRIOR FILING DATE: 1991-03-18
: NUMBER OF SEQ ID NOS: 19
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1
: LENGTH: 157
: TYPE: prt
: ORGANISM: Homo sapiens
: US-09-766-535A-1

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Query Match      100.0%; Score 89; DB 10; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 YSQVLEKGGCCPSTHV 16
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Db 59 YSQVLEKGGCCPSTHV 74

Db 59 YSQVLFKGGCPSTHV 74

RESULT 13

US-09-854-208-19
; Sequence 19, Application US/09854208
; Patent No. US20020106743A1

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; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Wood, William I.
; GENERAL INFORMATION:
; Account No.: 08A90601007474JA1

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Query Match      100.0%; Score 89; DB 10; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 16: Conservative 0; Mismatches 0; Indels
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Qy 1 YSQVLFKQGCPSTHV 16
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Db 59 YSOVLFKGOGCPSTHV 74

Db 59 YSOVLFKGOGCPSTHV 74

RESULT 1A

RESULT 14
US-09-756-161A-1
; Sequence 1, Application US/09756161A
; Patent No. US20020132307A1

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; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; PRIOR FILING DATE: 1991-03-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0

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Query Match      100.0%; Score 89; DB 10; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels
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Db	59	YSQVLFKGGCPSTHV	74

Db 59 YSQVLFKGGCPSTHV 74

RESULT 15

US-10-010-229-1
; Sequence 1, Application US/10010229
; Patent No. US20020114805A1

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> GENERAL INFORMATION:
> APPLICANT: Le, Junming
> APPLICANT: Vilcek, Jan
> APPLICANT: Daddona, Peter
> APPLICANT: Chrayeb, John
> APPLICANT: Knight, David M.
> APPLICANT: Siegel, Scott
> TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
> TITLE OF INVENTION: Human Tumor Necrosis Factor
> FILE REFERENCE: 0975.1005-013
> CURRENT APPLICATION NUMBER: US/10/010,229
> CURRENT FILING DATE: 2001-12-07
> PRIOR APPLICATION NUMBER: US/09/927,703
> PRIOR FILING DATE: 2001-08-10
> NUMBER OF SEQ ID NOS: 19
> SOFTWARE: FastSeq for Windows version 4.0

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Query Match	100.0%;	Score 89;	DB 12;	Length 157;
Best Local Similarity	100.0%;	Pred. No. 1.1e-07;		
Matches 16:	Conservative 0;	Mismatches 0;	Indels 0;	

QY 1 YSQVLFKGGCPSTHV 16
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59 YSQVLFKGGCPSTHV 74
pb

59 YSQVLEKGGGCPSTHY 74

Search completed: December 4, 2002, 13:30:34
Job time : 5.89474 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 4, 2002, 13:21:18 ; Search time 9.68421 Seconds
(without alignments)
48.612 Million cell updates/sec

Title: US-09-754-004-1

Perfect score: 89

Sequence: 1 YSQLFKGGGCPSTHV 16

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Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued_Patents_AA:*
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 - 2: /cgn2.6/ptodata/1/iaa/5B_COMB.pep.*
 - 3: /cgn2.6/ptodata/1/iaa/6A_COMB.pep.*
 - 4: /cgn2.6/ptodata/1/iaa/6B_COMB.pep.*
 - 5: /cgn2.6/ptodata/1/iaa/PCUS_COMB.pep.*
 - 6: /cgn2.6/ptodata/1/iaa/backfiles1.pep.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	89	100.0	22	4	US-08-690-775-1
2	89	100.0	139	1	US-07-994-469A-10
3	89	100.0	145	1	US-07-994-469A-9
4	89	100.0	147	1	US-07-668-517-1
5	89	100.0	147	4	US-09-105-343A-9
6	89	100.0	148	1	US-07-668-517-2
7	89	100.0	148	1	US-07-668-517-15
8	89	100.0	149	1	US-07-668-517-3
9	89	100.0	149	1	US-07-668-517-16
10	89	100.0	150	1	US-07-668-517-4
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12	89	100.0	150	1	US-07-668-517-6
13	89	100.0	150	1	US-07-668-517-8
14	89	100.0	150	1	US-07-668-517-9
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16	89	100.0	150	1	US-07-668-517-11
17	89	100.0	150	1	US-07-668-517-12
18	89	100.0	150	1	US-07-668-517-13
19	89	100.0	150	1	US-07-668-517-14
20	89	100.0	150	1	US-07-668-517-17
21	89	100.0	150	1	US-07-668-517-29
22	89	100.0	150	1	US-07-668-517-31
23	89	100.0	150	1	US-07-668-517-35
24	89	100.0	150	1	US-07-668-517-37
25	89	100.0	150	1	US-07-994-469A-6
26	89	100.0	150	1	US-07-994-469A-7
27	89	100.0	150	1	US-07-994-469A-8

28 89 100.0 150 1 US-07-994-469A-57 Sequence 57, Appl
29 89 100.0 150 4 US-09-286-529-25 Sequence 25, Appl
30 89 100.0 151 1 US-07-668-517-7 Sequence 7, Appl
31 89 100.0 151 1 US-07-668-517-18 Sequence 18, Appl
32 89 100.0 151 1 US-07-668-517-19 Sequence 19, Appl
33 89 100.0 151 1 US-07-668-517-20 Sequence 20, Appl
34 89 100.0 151 1 US-07-668-517-22 Sequence 22, Appl
35 89 100.0 151 1 US-07-668-517-23 Sequence 23, Appl
36 89 100.0 151 1 US-07-668-517-24 Sequence 24, Appl
37 89 100.0 151 1 US-07-668-517-25 Sequence 25, Appl
38 89 100.0 151 1 US-07-668-517-26 Sequence 26, Appl
39 89 100.0 151 1 US-07-668-517-27 Sequence 27, Appl
40 89 100.0 151 1 US-07-668-517-28 Sequence 28, Appl
41 89 100.0 151 1 US-07-668-517-30 Sequence 30, Appl
42 89 100.0 151 1 US-07-668-517-32 Sequence 32, Appl
43 89 100.0 151 1 US-07-668-517-36 Sequence 36, Appl
44 89 100.0 151 1 US-07-668-517-38 Sequence 38, Appl
45 89 100.0 152 1 US-07-668-517-21 Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-08-690-775-1
; Sequence 1, Application US/08690775
; Patent No. 6270766
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Marc
; TITLE OF INVENTION: ANTI-TNF ANTIBODIES AND METHOTREXATE IN
; TITLE OF INVENTION: THE TREATMENT OF AUTOIMMUNE DISEASE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: TWO MILITIA DRIVE
; CITY: LEXINGTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/690,775
; FILING DATE: 01-AUG-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/607,419
; FILING DATE: 28-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/02070
; FILING DATE: 06-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB94/00462
; FILING DATE: 15-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/02070
; FILING DATE: 06-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/958,248
; FILING DATE: 08-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook Esq., David E
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: KIR92-01A4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS:

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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-690-775-1

Query Match      100.0%; Score 89; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.7e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSQVLFKGGGCPSTHV 16
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Db 1 YSQVLFKGGGCPSTHV 16

RESULT 2
US-07-994-469A-10
; Sequence 10, Application US/07994469A
; Patent No. 5519119
; GENERAL INFORMATION:
; APPLICANT: Yamada, No. 5519119utoshi
; APPLICANT: Kato, Masanari
; APPLICANT: Miyata, Keizo
; APPLICANT: Aoyama, Yoshiyuki
; APPLICANT: Shikama, Hiroshi
; TITLE OF INVENTION: Polypeptide
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/994,469A
; FILING DATE: 21-DEC-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5519119man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 72-085-0 FWC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)413-3000
; TELEFAX: (703)413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-994-469A-10

Query Match      100.0%; Score 89; DB 1; Length 139;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSQVLFKGGGCPSTHV 16
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Db 49 YSQVLFKGGGCPSTHV 64

RESULT 3
US-07-994-469A-9
; Sequence 9, Application US/07994469A
; Patent No. 5519119
; GENERAL INFORMATION:
; APPLICANT: Yamada, No. 5519119utoshi
; APPLICANT: Kato, Masanari
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; APPLICANT: Miyata, Keizo
; APPLICANT: Aoyama, Yoshiyuki
; APPLICANT: Shikama, Hiroshi
; TITLE OF INVENTION: Polypeptide
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/994,469A
; FILING DATE: 21-DEC-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5519119man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 72-085-0 FWC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)413-3000
; TELEFAX: (703)413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 145 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-994-469A-9

Query Match      100.0%; Score 89; DB 1; Length 145;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSQVLFKGGGCPSTHV 16
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Db 55 YSQVLFKGGGCPSTHV 70

RESULT 4
US-07-668-517-1
; Sequence 1, Application US/07668517
; Patent No. 5262309
; GENERAL INFORMATION:
; APPLICANT: Satoshi NAKAMURA et al.
; TITLE OF INVENTION: No. 5262309el Physiologically Active
; TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism
; TITLE OF INVENTION: Cell, Pharmaceutical Composition and Method of Recovering
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/668,517
; FILING DATE: 19910322
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
```

```
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Matthew Jacob
; REGISTRATION NUMBER: 25,154
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX: 202-371-8856
;
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 147 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
;
; US-07-668-517-1
;
; Query Match 100.0%; Score 89; DB 1; Length 147;
; Best Local Similarity 100.0%; Pred. No. 1.3e-07;
; Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 YSQVLFKGGGCPSTHV 16
; Db 49 YSQVLFKGGGCPSTHV 64
;
; RESULT 5
; US-09-105-343A-9
; Sequence 9, Application US/09105343A
; Patent No. 6207642
; GENERAL INFORMATION:
; APPLICANT: WILEY, S.R.
; TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL
; TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-6050
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/105,343A
; FILING DATE: 12-FEB-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/02859
; FILING DATE: 12-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: BECKER, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6048.US.P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-935-1729
; TELEFAX: 847-938-2623
; TELEX:
;
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 147 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
```

```
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6207642e
; US-09-105-343A-9
;
; Query Match 100.0%; Score 89; DB 4; Length 147;
; Best Local Similarity 100.0%; Pred. No. 1.3e-07;
; Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 YSQVLFKGGGCPSTHV 16
; Db 50 YSQVLFKGGGCPSTHV 65
;
; RESULT 6
; US-07-668-517-2
; Sequence 2, Application US/07668517
; Patent No. 5262309
; GENERAL INFORMATION:
; APPLICANT: Satoshi NAKAMURA et al.
; TITLE OF INVENTION: No. 5262309el Physiologically Active
; TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism
; TITLE OF INVENTION: Cell, Pharmaceutical Composition and Method of Recovering
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/668,517
; FILING DATE: 19910322
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Matthew Jacob
; REGISTRATION NUMBER: 25,154
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX: 202-371-8856
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 148 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
;
; US-07-668-517-2
;
; Query Match 100.0%; Score 89; DB 1; Length 148;
; Best Local Similarity 100.0%; Pred. No. 1.3e-07;
; Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 YSQVLFKGGGCPSTHV 16
; Db 50 YSQVLFKGGGCPSTHV 65
;
; RESULT 7
```

US-07-668-517-15
; Sequence 15, Application US/07668517
; Patent No. 5262309
; GENERAL INFORMATION:
; APPLICANT: Satoshi NAKAMURA et al.
; TITLE OF INVENTION: No. 5262309el Physiologically Active
; TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism
; TITLE OF INVENTION: Cell, Pharmaceutical Composition and Method of Recovering
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/668,517
; FILING DATE: 19910322
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Matthew Jacob
; REGISTRATION NUMBER: 25,154
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX: 202-371-8856
; TELEX:
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 148 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
US-07-668-517-15
Query Match 100.0%; Score 89; DB 1; Length 148;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YSQVLFKGQGCPSSTHV 16
Db 50 YSQVLFKGQGCPSSTHV 65
RESULT 8
US-07-668-517-3
; Sequence 3, Application US/07668517
; Patent No. 5262309
; GENERAL INFORMATION:
; APPLICANT: Satoshi NAKAMURA et al.
; TITLE OF INVENTION: No. 5262309el Physiologically Active
; TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism
; TITLE OF INVENTION: Cell, Pharmaceutical Composition and Method of Recovering
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.

COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/668,517
FILING DATE: 19910322
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Matthew Jacob
REGISTRATION NUMBER: 25,154
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 149 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-07-668-517-3
Query Match 100.0%; Score 89; DB 1; Length 149;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YSQVLFKGQGCPSSTHV 16
Db 51 YSQVLFKGQGCPSSTHV 66
RESULT 9
US-07-668-517-16
; Sequence 16, Application US/07668517
; Patent No. 5262309
; GENERAL INFORMATION:
; APPLICANT: Satoshi NAKAMURA et al.
; TITLE OF INVENTION: No. 5262309el Physiologically Active
; TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism
; TITLE OF INVENTION: Cell, Pharmaceutical Composition and Method of Recovering
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/668,517
; FILING DATE: 19910322
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Matthew Jacob
REGISTRATION NUMBER: 25,154
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 149 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-07-668-517-16

Query Match 100.0%; Score 89; DB 1; Length 149;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSQVLFKGGCGPSTHV 16
|||||
DB 51 YSQVLFKGGCGPSTHV 66

RESULT 10
US-07-668-517-4
Sequence 4, Application US/07668517
Patent No. 5262309
GENERAL INFORMATION:
APPLICANT: Satoshi NAKAMURA et al.
TITLE OF INVENTION: No. 5262309el Physiologically Active
TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism
TITLE OF INVENTION: Cell, Pharmaceutical Composition and Method of Recovering
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/668,517
FILING DATE: 19910322
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Matthew Jacob
REGISTRATION NUMBER: 25,154
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 150 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear

Query Match 100.0%; Score 89; DB 1; Length 150;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSQVLFKGGCGPSTHV 16
|||||
DB 52 YSQVLFKGGCGPSTHV 67

FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-07-668-517-4

Query Match 100.0%; Score 89; DB 1; Length 150;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSQVLFKGGCGPSTHV 16
|||||
DB 52 YSQVLFKGGCGPSTHV 67

RESULT 11
US-07-668-517-5
Sequence 5, Application US/07668517
Patent No. 5262309
GENERAL INFORMATION:
APPLICANT: Satoshi NAKAMURA et al.
TITLE OF INVENTION: No. 5262309el Physiologically Active
TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism
TITLE OF INVENTION: Cell, Pharmaceutical Composition and Method of Recovering
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/668,517
FILING DATE: 19910322
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Matthew Jacob
REGISTRATION NUMBER: 25,154
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 150 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-07-668-517-5

Query Match 100.0%; Score 89; DB 1; Length 150;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSQVLFKGGCGPSTHV 16
|||||
DB 52 YSQVLFKGGCGPSTHV 67

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Matthew Jacob
;; REGISTRATION NUMBER: 25,154
;; REFERENCE/DOCKET NUMBER:
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-8850
;; TELEFAX: 202-371-8856
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 150 amino acids
;; TYPE: AMINO ACID
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; FEATURE:
;; NAME/KEY:
;; LOCATION:
;; IDENTIFICATION METHOD:
;; OTHER INFORMATION:
;; US-07-668-517-9

Query Match 100.0%; Score 89; DB 1; Length 150;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSQVLFKGGGCPSTHV 16
| | | | | | | | | | | | | | | | | |
Db 52 YSQVLFKGGGCPSTHV 67

RESULT 15

US-07-668-517-10
; Sequence 10, Application US/07668517
; Patent No. 5262309
; GENERAL INFORMATION:
; APPLICANT: Satoshi NAKAMURA et al.
; TITLE OF INVENTION: No. 5262309el Physiologically Active
; TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism
; TITLE OF INVENTION: Cell, Pharmaceutical Composition and Method of Recovering
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/668,517
; FILING DATE: 19910322
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Matthew Jacob
; REGISTRATION NUMBER: 25,154
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX: 202-371-8856
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 150 amino acids

;; TYPE: AMINO ACID
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; FEATURE:
;; NAME/KEY:
;; LOCATION:
;; IDENTIFICATION METHOD:
;; OTHER INFORMATION:
;; US-07-668-517-10
Query Match 100.0%; Score 89; DB 1; Length 150;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YSQVLFKGGGCPSTHV 16
| | | | | | | | | | | | | | | | | |
Db 52 YSQVLFKGGGCPSTHV 67
Search completed: December 4, 2002, 13:24:28
Job time : 9.68421 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 4, 2002, 13:21:33 ; Search time 15.6316 Seconds
(without alignments)
135.300 Million cell updates/sec

Title: US-09-754-004-2

Perfect score: 115

Sequence: 1 YQTKVNLSSAIPQCQRETPG 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR-73.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	115	100.0	232	1 S12606	tumor necrosis fac
2	115	100.0	233	1 QW0UN	tumor necrosis fac
3	115	100.0	233	1 S22052	tumor necrosis fac
4	115	100.0	233	2 S11688	tumor necrosis fac
5	102	88.7	185	2 S52715	tumor necrosis fac
6	102	88.7	193	2 S06192	tumor necrosis fac
7	102	88.7	233	1 S24642	tumor necrosis fac
8	98	85.2	234	1 JH0529	tumor necrosis fac
9	97	84.3	235	2 I54490	tumor necrosis fac
10	96	83.5	235	1 QWMSN	tumor necrosis fac
11	93	80.9	234	1 A25451	tumor necrosis fac
12	92	80.0	235	2 JU0029	tumor necrosis fac
13	84	73.0	234	1 J01344	tumor necrosis fac
14	46	40.0	704	2 T02558	hypothetical prote
15	44	38.3	179	2 B72612	hypothetical prote
16	44	38.3	396	2 A90107	putative nucleolar
17	44	38.3	889	2 T11742	egg sperm receptor
18	44	38.3	1122	2 B26427	period clock prote
19	44	38.3	1218	2 A26427	period clock prote
20	43.5	37.8	230	2 J31722	hypothetical prote
21	43.5	37.8	329	2 JC4093	signal recognition
22	43	37.4	70	2 JV0103	hypothetical 8.5K
23	43	37.4	156	2 T33725	ribonuclease H (EC
24	43	37.4	157	2 S48701	coat protein, 18K
25	43	37.4	182	2 A72240	conserved hypothet
26	43	37.4	934	2 T39941	hypothetical prote
27	42	36.5	157	2 S65055	coat protein - Chi
28	42	36.5	235	2 T33962	hypothetical prote
29	42	36.5	266	2 T31217	transcription regu

30 42 36.5 290 1 XYCHY3
31 42 36.5 340 2 A97037
32 42 36.5 418 2 T00813
33 42 36.5 458 2 A26940
34 42 36.5 475 2 D83202
35 42 36.5 846 2 JC7720
36 42 36.5 848 2 E86443
37 42 36.5 1218 2 A25018
38 42 36.5 1218 2 A26588
39 42 36.5 1400 1 I38185
40 41.5 36.1 1615 2 JC6510
41 41 35.7 146 2 H97453
42 41 35.7 146 2 AB2672
43 41 35.7 160 2 A82020
44 41 35.7 345 2 S36518
45 41 35.7 540 2 T26445

ALIGNMENTS

RESULT 1

S12606

tumor necrosis factor alpha precursor - pig

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 10-Sep-1999 #sequence-revision 10-Sep-1999 #text_change 04-Feb-2000

C:Accession: S12606; S17290; S18965; I46659

R:Drews, R.T.; Coffee, B.W.; Prestwood, A.K.; McGraw, R.A.

Nucleic Acids Res. 18, 5564, 1990

A:Title: Gene sequence of porcine tumor necrosis factor alpha.

A:Reference number: S12606; MUID:91016861; PMID:2216741

A:Accession: S12606

A:Molecule type: DNA

A:Residues: 1-232 <DRE>

A:Cross-references: EMBL:X54001; NID:g2135; PIDN:CAA37949.1; PID:g2136

R:Kuhnert, P.; Wuehrich, C.; Peterhans, E.; Pauli, U.

Gene 102, 171-178, 1991

A:Title: The porcine tumor necrosis factor-encoding genes: sequence and comparative a

A:Reference number: S17289; MUID:91340150; PMID:1874444

A:Accession: S17290

A:Molecule type: DNA

A:Residues: 1-232 <KUHF>

A:Cross-references: EMBL:X54859; NID:g2132; PIDN:CAA38639.1; PID:g2134

A:Note: the authors translated the codon GAG for residue 202 as Gly

R:Choi, C.S.; Molitor, T.W.; Lin, G.F.; Murtaugh, M.P.

Submitted to the EMBL Data Library, January 1991

A:Description: Complete nucleotide sequence of a cDNA encoding porcine tumor necrosis

A:Reference number: S18965

A:Accession: S18965

A:Molecule type: mRNA

A:Residues: 1-232 <CHO>

A:Cross-references: EMBL:X57321; NID:g2137; PIDN:CAA40591.1; PID:g2138

R:Pauli, U.; Beutler, B.; Peterhans, E.

Gene 81, 185-191, 1989

A:Title: Porcine tumor necrosis factor alpha: Cloning with the polymerase chain react

A:Reference number: I46659; MUID:90034181; PMID:2478420

A:Accession: I46659

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 44-232 <PAU>

A:Cross-references: GB:M29079; NID:gl64694; PIDN:AAA31128.1; PID:gl64695

C:Genetics:

A:Introns: 62/3; 78/1; 93/1

C:Superfamily: tumor necrosis factor

C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; m

F:1-77/Domain: propeptide #status predicted <PRO>

F:78-232/Product: tumor necrosis factor alpha #status predicted <PRO>

F:19,20/Binding site: myristate (Lys) (covalent) #status predicted

F:81/Binding site: carbohydrate (Ser) (covalent) #status predicted

F:144-176/Bisulfide bonds: #status predicted

Query Match

Best Local Similarity 100.0%; Score 115; DB 1; Length 232;

Pred. No. 3e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YQTKVNLISAIKSPCQRETPEG 22
 |||||||||||||||||||

DB 162 YQTKVNLISAIKSPCQRETPEG 183

RESULT 2

QMHUN
 tumor necrosis factor alpha precursor [validated] - human
 N:Alternative names: cachectin; TNFA
 C:Species: Homo sapiens (man)
 C:Date: 28-Aug-1985 #sequence-revision 28-Aug-1985 #text-change 08-Dec-2000
 C:Accession: A93585; S36153; A93351; A44189; B61478; S62610; S54522; A01646; B23
 R:Newwin, G.E.; Naylor, S.L.; Sakauchi, A.Y.; Smith, D.; Jarrett-Nedwin, J.; Pennica, D.
 Nucleic Acids Res. 13, 6361-6373, 1985
 A:Title: Human lymphotoxin and tumor necrosis factor genes: structure, homology and chr
 A:Reference number: A93585; MUID:86016093; PMID:2995927
 A:Accession: A93585
 A:Molecule type: DNA
 A:Residues: 1-233 <NED>
 A:Cross-references: GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210
 R:Riris, F.J.M.; Bougueleret, L.; Prieur, S.; Caterina, D.; Primas, G.; Perrot, V.; Jurka
 Nature Genet. 3, 137-145, 1993
 A:Title: Dense Alu clustering and a potential new member of the NFkappaB family within a
 A:Reference number: S36152; MUID:93272029; PMID:8499947
 A:Accession: S36153
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-233 <IRI>
 A:Cross-references: EMBL:Z15026; NID:g37211; PIDN:CAA78745.1; PID:g37212
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
 R:Pennica, D.; Nedwin, G.E.; Hayflick, J.S.; Seeburg, P.H.; Derynck, R.; Palladino, M.A.
 Nature 312, 724-729, 1984
 A:Title: Human tumour necrosis factor: precursor structure, expression and homology to 1
 A:Reference number: A93351; MUID:85086244; PMID:6392892
 A:Accession: A93351
 A:Molecule type: mRNA
 A:Residues: 1-233 <PEN>
 A:Cross-references: GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210
 A:Note: this protein was isolated from the monocyte-like cell line HL-60 from a promyeloc
 R:Wang, A.M.; Creasey, A.A.; Ladner, M.B.; Lin, L.S.; Strickler, J.; Van Arsdell, J.N.;
 Science 228, 149-154, 1985
 A:Title: Molecular cloning of the complementary DNA for human tumor necrosis factor.
 A:Reference number: A44189; MUID:85142190; PMID:3856324
 A:Accession: A44189
 A:Molecule type: mRNA
 A:Residues: 1-62, S', 64-233 <WAN>
 A:Cross-references: GB:M10988; NID:g339737; PIDN:AAA61198.1; PID:g339738
 R:Fukuda, S.; Ando, S.; Sanou, O.; Tani, M.; Fujii, M.; Masaki, N.; Nakamura, K.I.; An
 Lymphokine Res. 7, 175-185, 1988
 A:Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta and
 A:Reference number: A61478; MUID:88301617; PMID:2841543
 A:Accession: B61478
 A:Molecule type: protein
 A:Residues: 83-102; 109-119; 121-128, X', 130-131; 142-144, X', 146, 'XXX', 150-152; 159-174; 180
 R:Marneout, A.; Fransen, L.; Tavernier, J.; Van Der Heyden, J.; Tizard, R.; Kawashima,
 Eur. J. Biochem. 152, 515-522, 1985
 A:Title: Molecular cloning and expression of human tumor necrosis factor and comparison
 A:Reference number: I53311; MUID:86030296; PMID:3932069
 A:Accession: I53311
 A:Status: translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-233 <MAR>
 A:Cross-references: GB:M26331; NID:g339763; PIDN:AAA36758.1; PID:g339764
 A:Experimental source: U-937 cells
 R:Takakura-Yamamoto, R.; Yamamoto, S.; Fukuda, S.; Kurimoto, M.
 Eur. J. Biochem. 235, 431-437, 1996
 A:Title: O-Glycosylated species of natural human tumor-necrosis factor-alpha.
 A:Reference number: S62610; MUID:96202967; PMID:8631363
 A:Accession: S62610
 A:Molecule type: protein
 A:Residues: 1-77-99 <TAK>

R:D'Alfonso, S.; Richiardi, P.M.
 Immunogenetics 39, 150-154, 1994
 A:Title: A polymorphic variation in a putative regulation box of the TNFA promoter re
 A:Reference number: I54522; MUID:94102809; PMID:7903959
 A:Accession: I54522
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-8 <DAL>
 A:Cross-references: GB:S68530; NID:g544751
 R:Stevenson, F.T.; Bursten, S.L.; Locksley, R.M.; Lovett, D.H.
 J. Exp. Med. 176, 1053-1062, 1992
 A:Title: Myristyl acylation of the tumor necrosis factor alpha precursor on specific
 A:Reference number: A59163; MUID:93018820; PMID:1402651
 A:Contents: annotation; identification of myristylated lysines
 R:Agarwal, B.B.; Kehr, W.J.; Hass, P.E.; Moffat, B.; Spencer, S.A.; Henzel, W.J.; Br
 J. Biol. Chem. 260, 2345-2354, 1985
 A:Title: Human tumor necrosis factor. Production, purification, and characterization.
 A:Reference number: A92511; MUID:85130974; PMID:3871770
 A:Contents: annotation; disulfide bond
 C:Comment: Secreted from mitogen-activated macrophages within 4-24 hours after induct
 out detriment to normal cells. It can also act synergistically with interferon gamma
 C:Comment: TNF-alpha and -beta (lymphotoxin) are the products of different genes clos
 ut are produced by different cell types and have different induction kinetics.
 C:Genetics:
 A:Gene: GDB:TNF; TNFA
 A:Cross-references: GDB:120441; OMIM:191160
 A:Map position: 6p21.3-6p21.3
 A:Introns: 62/3; 78/1; 94/1
 C:Complex: homotrimer
 C:Superfamily: tumor necrosis factor
 C:Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lipoprotein; lymphokine; m
 F:1-76/Domain: propeptide #status predicted <PRO>
 F:77-233/Product: tumor necrosis factor #status experimental <MAT>
 F:19,20/Binding site: myristate (Lys) (covalent) #status experimental
 F:81/Binding site: carbohydrate (Ser) (covalent) (partial) #status experimental
 F:145-177/Disulfide bonds: #status experimental

Query Match 100.0%; Score 115; DB 1; Length 233;
 Best Local Similarity 100.0%; Pred. No. 3e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YQTKVNLISAIKSPCQRETPEG 22
 |||||||||||||||||||

DB 163 YQTKVNLISAIKSPCQRETPEG 184

RESULT 3

S22052
 tumor necrosis factor alpha precursor - baboon
 C:Species: Papio sp. (baboon)
 C:Date: 10-Sep-1999 #sequence-revision 10-Sep-1999 #text-change 04-Feb-2000
 C:Accession: S22052
 R:Sanjanwalla, M.; Edwards, A.
 submitted to the EMBL Data Library, September 1991
 A:Description: Baboon Tumor Necrosis Factor Derived from Sequences of Genomic DNA.
 A:Reference number: S22052
 A:Accession: S22052
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-233 <SAN>
 A:Cross-references: EMBL:X62141; NID:g38159; PIDN:CAA44068.1; PID:g38160
 C:Genetics:
 A:Introns: 62/3; 78/1; 94/1
 C:Superfamily: tumor necrosis factor
 C:Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein
 F:19,20/Binding site: myristate (Lys) (covalent) #status predicted
 F:81/Binding site: carbohydrate (Ser) (covalent) #status predicted
 F:145-177/Disulfide bonds: #status predicted

Query Match 100.0%; Score 115; DB 1; Length 233;
 Best Local Similarity 100.0%; Pred. No. 3e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YQTKVNLLSAIKSPCQRETPEG 22
|||||
Db 163 YQTKVNLLSAIKSPCQRETPEG 184

RESULT 4

S11688
tumor necrosis factor alpha precursor - cat
C:Species: Felis silvestris catus (domestic cat)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 04-Feb-2000
C:Accession: S11688
R:McGraw, R.A.; Coffee, B.W.; Otto, C.M.; Drews, R.T.; Rawlings, C.A.
Nucleic Acids Res. 18, 5563, 1990
A:Title: Gene sequence of feline tumor necrosis factor alpha.
A:Reference number: S11688; MUID:91016860; PMID:2216740
A:Accession: S11688
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-233 <MCG>
A:Cross-references: EMBL:X54000; NID:g1084; PIDN:CAA37948.1; PID:g295777
C:Genetics:
A:Introns: 62/3; 78/1; 94/1
C:Superfamily: tumor necrosis factor
C:Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein
F:19/20/Binding site: myristate (Lys) (covalent) #status predicted
F:81/Binding site: carbohydrate (Ser) (covalent) #status predicted
F:145-177/Disulfide bonds: #status predicted

Query Match 100.0%; Score 115; DB 2; Length 233;
Best Local Similarity 100.0%; Pred. No. 3e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YQTKVNLLSAIKSPCQRETPEG 22
|||||
Db 163 YQTKVNLLSAIKSPCQRETPEG 184

RESULT 5

S52715
tumor necrosis factor alpha precursor - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 04-Feb-2000
C:Accession: S52715
R:Metzger, B.; Gaidulis, L.
Submitted to the EMBL Data Library, March 1995
A:Description: Cloning and sequence analysis of cDNAs encoding bovine CD40 ligand and bo
A:Reference number: S52715
A:Accession: S52715
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-185 <MER>
A:Cross-references: EMBL:Z48808; NID:g755701; PIDN:CAA88743.1; PID:g755702
C:Superfamily: tumor necrosis factor
C:Keywords: glycoprotein
F:33/Binding site: carbohydrate (Ser) (covalent) #status predicted
F:97-129/Disulfide bonds: #status predicted

Query Match 88.7%; Score 102; DB 2; Length 185;
Best Local Similarity 90.5%; Pred. No. 3.3e-09;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YQTKVNLLSAIKSPCQRETPE 21
|||||
Db 115 YQTKVNLLSAIKSPCHRETPE 135

RESULT 6

S06192
tumor necrosis factor alpha precursor - goat (fragment)
N:Alternate names: cachectin; TNF alpha
C:Species: Capra aegagrus hircus (domestic goat)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 31-Jan-2000
C:Accession: S06192; S41867

R:Goldstein, I.M.; Henner, D.; Talhouk, A.
Submitted to the EMBL Data Library, March 1989
A:Reference number: S06192
A:Accession: S06192
A:Molecule type: mRNA
A:Residues: 1-193 <GOL>
A:Cross-references: EMBL:X14828; NID:g992; PIDN:CAA32937.1; PID:g993
R:Rimstad, E.
Submitted to the EMBL Data Library, January 1994
A:Reference number: S41867
A:Accession: S41867
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 36-38,'S',40-78,'A',80-88,'N',90-114,'O',116-123,'D',125-144,'G',145-173,'
A:Cross-references: EMBL:X77317; NID:g452607; PIDN:CAA54523.1; PID:g452608
C:Superfamily: tumor necrosis factor
C:Keywords: cytokine; cytotoxin; glycoprotein; lymphokine; macrophage; membrane prote
F:42/Binding site: carbohydrate (Ser) (covalent) #status predicted
F:106-138/Disulfide bonds: #status predicted

Query Match 88.7%; Score 102; DB 2; Length 193;
Best Local Similarity 90.5%; Pred. No. 3.5e-09;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YQTKVNLLSAIKSPCQRETPE 21
|||||
Db 124 YQTKVNLLSAIKSPCHRETPE 144

RESULT 7

S24642
tumor necrosis factor alpha precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C:Accession: I46047; S24642
R:Cludts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.; Droogmans, L.
Cytokine 5, 336-341, 1993
A:Title: Cloning and characterization of the tandemly arranged bovine lymphotoxin and
A:Reference number: I46046; MUID:94083525; PMID:8260599
A:Accession: I46047
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-233 <CL2>
A:Cross-references: EMBL:Z14137; NID:g796; PIDN:CAA78511.1; PID:g798
C:Genetics:
A:Gene: TNFA
A:Introns: 62/3; 78/1; 94/1
C:Superfamily: tumor necrosis factor
C:Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein
F:20/Binding site: myristate (Lys) (covalent) #status predicted
F:81/Binding site: carbohydrate (Ser) (covalent) #status predicted
F:145-177/Disulfide bonds: #status predicted

Query Match 88.7%; Score 102; DB 1; Length 233;
Best Local Similarity 90.5%; Pred. No. 4.2e-09;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YQTKVNLLSAIKSPCQRETPE 21
|||||
Db 163 YQTKVNLLSAIKSPCHRETPE 183

RESULT 8

JH0529
tumor necrosis factor alpha precursor - sheep
N:Alternate names: cachectin; TNF alpha
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C:Accession: JH0529; S48118; S13114; S20661
R:Green, I.R.; Sargan, D.R.
Gene 109, 203-210, 1991
A:Title: Sequence of the cDNA encoding ovine tumor necrosis factor-alpha: problems wi
A:Reference number: JH0529; MUID:92112044; PMID:1765267

A:Accession: JH0529
A:Molecule type: mRNA
A:Residues: 1-234 <GRE>
A:Cross-references: EMBL:X55152; NID:g1405; PIDN:CAA38952.1; PID:g1406
A:Experimental source: alveolar macrophage
R:Nash, A.D.; Barcham, G.J.; Brandon, M.R.; Andrews, A.E.
Immunol. Cell Biol. 69, 273-283, 1991
A:Title: Molecular cloning, expression and characterization of ovine TNF-alpha.
A:Reference number: S48118; MUID:92155784; PMID:1786996
A:Accession: S48118
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-234 <NAS>
A:Cross-references: EMBL:X56756; NID:g297806; PIDN:CAA40076.1; PID:g297807
R:Young, A.J.; Hay, J.B.; Chan, J.Y.C.
Nucleic Acids Res. 18, 6723, 1990
A:Title: Primary structure of ovine tumor necrosis factor alpha cDNA.
A:Reference number: S13114; MUID:91067496; PMID:2251151
A:Accession: S13114
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-62,64-234 <YOU>
A:Cross-references: EMBL:X55966; NID:g1403; PIDN:CAA39437.1; PID:g1404
A:Note: comparison with the introns of homologous sequences suggest that this is probably
C:Superfamily: tumor necrosis factor
C:Keywords: alternative splicing; cytokine; cytotoxin; glycoprotein; lipoprotein; lympho
F:1-77/Domain: propeptide #status predicted <PRO>
F:78-234/Product: tumor necrosis factor alpha #status predicted <TUM>
F:20/Binding site: myristate (Lys) (covalent) #status predicted
F:82/Binding site: carbohydrate (Ser) (covalent) #status predicted
F:96/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:146-178/Disulfide bonds: #status predicted

Query Match 85.2%; Score 98; DB 1; Length 234;
Best Local Similarity 86.4%; Pred. No. 1.9e-08;
Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YQTKVNLLSAIKSPCORETPEG 22
|||||:||||| ||| ||
DB 164 YQTKVNLLSAIKSPCHRETLEG 185

RESULT 9
I54490
tumor necrosis factor alpha precursor - white-footed mouse
C:Species: Peromyscus leucopus (white-footed mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 04-Feb-2000
C:Accession: I54490
R:Crew, M.D.; Filipowsky, M.E.
Immunogenetics 35, 351-353, 1992
A:Title: Sequence of the tumor necrosis factor/cachectin (TNF) gene from Peromyscus leu
A:Reference number: I54490; MUID:92218012; PMID:1348497
A:Accession: I54490
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-235 <RES>
A:Cross-references: GB:M59233; NID:g202506; PIDN:AAA40596.1; PID:g202507
C:Genetics:
A:Gene: PTNF
A:Introns: 62/3; 81/1; 97/1
C:Superfamily: tumor necrosis factor
C:Keywords: glycoprotein; lipoprotein; myristylation
F:19,20/Binding site: myristate (Lys) (covalent) #status predicted
F:84/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 84.3%; Score 97; DB 2; Length 235;
Best Local Similarity 81.8%; Pred. No. 2.9e-08;
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YQTKVNLLSAIKSPCORETPEG 22
|: ||||| ||||| : |||||
DB 165 YQTKVNLLSAIKSPCHRETPEG 186

RESULT 10
QWMSN
tumor necrosis factor alpha precursor - mouse
N:Alternate names: cachectin; TNF alpha
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 04-Feb-2000
C:Accession: A22908; S03791; A23127; A34251; I59058; A36696
R:Shiral, T.; Shimizu, N.; Shiojiri, S.; Horiguchi, S.; Ito, H.
DNA 7, 193-201, 1988
A:Title: Cloning and expression in Escherichia coli of the gene for mouse tumor necro
A:Reference number: A22908; MUID:88224564; PMID:2836146
A:Accession: A22908
A:Molecule type: DNA
A:Residues: 1-235 <SHI>
A:Cross-references: GB:M20155
R:Shakhov, A.N.; Nedospasov, S.A.
Biochim. Khim. 13, 701-705, 1987
A:Title: Molecular cloning of the genes coding for tumor necrosis factors: complete n
A:Reference number: S03791; MUID:87298639; PMID:3040015
A:Accession: S03791
A:Molecule type: DNA
A:Residues: 1-235 <SHA>
A:Cross-references: GB:M38296; NID:g202086; PIDN:AAA40459.1; PID:g202087
A:Note: article in Russian with English abstract
R:Semon, D.; Kawashima, E.; Jongeneel, C.V.; Shakhov, A.N.; Nedospasov, S.A.
Nucleic Acids Res. 15, 9083-9084, 1987
A:Title: Nucleotide sequence of the murine TNF locus, including the TNF-alpha-(tumor
A:Reference number: A93679; MUID:88067722; PMID:3684584
A:Accession: A27303
A:Molecule type: DNA
A:Residues: 1-235 <SEM>
R:Pennica, D.; Hayflick, J.S.; Bringman, T.S.; Palladino, M.A.; Goeddel, D.V.
Proc. Natl. Acad. Sci. U.S.A. 82, 6060-6064, 1985
A:Title: Cloning and expression in Escherichia coli of the cDNA for murine tumor necr
A:Reference number: A25164; MUID:85298296; PMID:38980078
A:Accession: A25164
A:Molecule type: mRNA
A:Residues: 1-235 <PEN>
A:Cross-references: GB:M11731; NID:g202084; PIDN:AAA40458.1; PID:g202085
R:Fransen, L.; Muller, R.; Marmenout, A.; Tavernier, J.; van der Heyden, J.; Kawashim
Nucleic Acids Res. 13, 4417-4429, 1985
A:Title: Molecular cloning of mouse tumour necrosis factor cDNA and its eukaryotic ex
A:Reference number: A23127; MUID:85242112; PMID:2989794
A:Accession: A23127
A:Molecule type: mRNA
A:Residues: 1-235 <FRA>
A:Cross-references: GB:X02611; NID:g54844; PIDN:CAA26457.1; PID:g54845
R:Cseh, K.; Beutler, B.
J. Biol. Chem. 264, 16256-16260, 1989
A:Title: Alternative cleavage of the cachectin/tumor necrosis factor propeptide resul
A:Reference number: A34251; MUID:89380231; PMID:2777790
A:Accession: A34251
A:Molecule type: protein
A:Residues: 70-87 <CSE>
R:Caput, D.; Beutler, B.; Hartog, K.; Thayer, R.; Brown-Shimer, S.L.; Cerami, A.
Proc. Natl. Acad. Sci. U.S.A. 83, 1670-1674, 1986
A:Title: Identification of a common nucleotide sequence in the 3'-untranslated region
A:Reference number: I59058; MUID:86149365; PMID:2419912
A:Accession: I59058
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-230,'R',232-235 <RES>
A:Cross-references: GB:M13049; NID:g202082; PIDN:AAA40457.1; PID:g202083
R:Sherry, B.; Jue, D.M.; Zentella, A.; Cerami, A.
Biochem. Biophys. Res. Commun. 173, 1072-1078, 1990
A:Title: Characterization of high molecular weight glycosylated forms of murine tumor
A:Reference number: A36696; MUID:91097531; PMID:2268312
A:Accession: A36696
A:Molecule type: protein
A:Residues: 80-85,'X',87-99 <SHE>
C:Genetics:

A;Introns: 62/3; 81/1; 97/1
A;Note: the first intron occurs in the 5'-untranslated region
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; memb
F;80-235/Product: tumor necrosis factor #status experimental <MAT>
F;20/Binding site: myristate (Lys) (covalent) #status predicted
F;84/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;86/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;148-179/Disulfide bonds: #status predicted

Query Match 83.58; Score 96; DB 1; Length 235;
Best Local Similarity 77.38; Pred. No. 4.2e-08;
Matches 17; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YQKVNLLSAIKSPCQRETPG 22
|| |||||:||||:||||
Db 165 YQKVNLLSAIKSPCKDTPG 186

RESULT 11
A25451
tumor necrosis factor alpha precursor - rabbit
N;Alternate names: cachectin; TNF alpha
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C;Accession: A25454; A25451; J50727
R;Ito, H.; Yamamoto, S.; Kuroda, S.; Sakamoto, H.; Kajihara, J.; Kiyota, T.; Hayashi, H.
DNA 5, 149-156, 1986
A;Title: Molecular cloning and expression in Escherichia coli of the cDNA coding for rat
A;Reference number: A25454; MUID:86219711; PMID:3519137
A;Accession: A25454
A;Molecule type: mRNA
A;Residues: 1-234 <ITO>
A;Cross-references: GB:M12845; NID:g165759; PIDN:AAA31486.1; PID:g165760
R;Ito, H.; Shirai, T.; Yamamoto, S.; Akira, M.; Kawahara, S.; Todd, C.W.; Wallace, R.B.
DNA 5, 157-165, 1986
A;Title: Molecular cloning of the gene encoding rabbit tumor necrosis factor.
A;Reference number: A25451; MUID:86219712; PMID:3519138
A;Accession: A25451
A;Molecule type: DNA
A;Residues: 1-234 <IT2>
A;Note: this sequence differs from that shown in having a Gln inserted between residues
R;Shakhov, A.N.; Kuprash, D.V.; Azizov, M.M.; Jongeneel, C.V.; Nedospasov, S.A.
Gene 95, 215-221, 1990
A;Title: Structural analysis of the rabbit TNF locus, containing the genes encoding TNF-
A;Reference number: JH0309; MUID:91065534; PMID:2249779
A;Accession: J50727
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-62,'Q',63-234 <SHA>
A;Cross-references: GB:M60340; GB:M35326; NID:g165754; PIDN:AAA31484.1; PID:g165756
C;Genetics:
A;Introns: 62/3; 80/1; 96/1
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; memb
F;1-81/Domain: propeptide #status predicted <PRO>
F;82-234/Product: tumor necrosis factor #status predicted
F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
F;83/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;147-178/Disulfide bonds: #status predicted

Query Match 80.98; Score 93; DB 1; Length 234;
Best Local Similarity 85.78; Pred. No. 1.3e-07;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YQKVNLLSAIKSPCQRETP 21
| | |||||:|||||
Db 164 YPKVNLLSAIKSCHRETP 184

RESULT 12
JU0029
tumor necrosis factor alpha precursor - rat

N;Alternate names: cachectin; TNF alpha
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 04-Feb-2000
C;Accession: JU0029; JN0868; S21674
R;Shirai, T.; Shimizu, N.; Horiguchi, S.; Ito, H.
Agric. Biol. Chem. 53, 1733-1736, 1989
A;Title: Cloning and expression in Escherichia coli of the gene for rat tumor necrosi
A;Reference number: JU0029
A;Accession: JU0029
A;Molecule type: DNA
A;Residues: 1-235 <SHI>
R;Kwon, J.; Chung, I.Y.; Benveniste, E.N.
Gene 132, 227-236, 1993
A;Title: Cloning and sequence analysis of the rat tumor necrosis factor-encoding gene
A;Reference number: JN0868; MUID:9404766; PMID:8224868
A;Accession: JN0868
A;Molecule type: DNA
A;Residues: 1-235 <KWO>
A;Cross-references: GB:L00981; NID:g205253; PIDN:AAA16275.1; PID:g205254
R;Estler, H.C.; Grewe, M.; Gausling, R.; Pavlovic, M.; Decker, K.
Biol. Chem. Hoppe-Seyler 373, 271-281, 1992
A;Title: Rat tumor necrosis factor-alpha. Transcription in rat Kupffer cells and in v
A;Reference number: S21674; MUID:92329007; PMID:1627266
A;Accession: S21674
A;Molecule type: mRNA
A;Residues: 1-38,'P',40-162,'T',164-201,'S',203-235 <EST>
A;Cross-references: GB:X66539; GB:S40199; NID:g395369; PIDN:CAA47146.1; PID:g395370
C;Comment: Tumor necrosis factor is secreted by macrophages in response to endotoxin
C;Genetics:
A;Gene: TNF-alpha
A;Introns: 62/3; 81/1; 97/1
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; m
F;80-235/Product: tumor necrosis factor #status predicted <MAT>
F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
F;84/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;86/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;148-179/Disulfide bonds: #status predicted

Query Match 80.08; Score 92; DB 2; Length 235;
Best Local Similarity 77.38; Pred. No. 1.9e-07;
Matches 17; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YQKVNLLSAIKSPCQRETPG 22
|| |||||:||||:||||
Db 165 YQKVNLLSAIKSPCKDTPG 186

RESULT 13
JQ1344
tumor necrosis factor alpha precursor - horse
N;Alternate names: cachectin; TNF alpha
C;Species: Equus caballus (domestic horse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C;Accession: JQ1344
R;Su, X.; Morris, D.D.; McGraw, R.A.
Gene 107, 319-321, 1991
A;Title: Cloning and characterization of gene TNF alpha encoding equine tumor necrosi
A;Reference number: JQ1344; MUID:92084125; PMID:1748301
A;Accession: JQ1344
A;Molecule type: DNA
A;Residues: 1-234 <SUX>
A;Cross-references: GB:M64087; NID:g164244; PIDN:AAA30959.1; PID:g164245
C;Comment: This protein is an important proximal mediator of endotoxemia.
C;Genetics:
A;Gene: TNF-alpha
A;Introns: 62/3; 79/1; 95/1
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; m
F;78-234/Product: tumor necrosis factor alpha #status predicted <TUN>
F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
F;82/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;146-178/Disulfide bonds: #status predicted

Query Match 73.0%; Score 84; DB 1; Length 234;
Best Local Similarity 76.2%; Pred. NO. 4e-06;
Matches 16; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 YOTKVNLLSAIKSPCORETPE 21
| : ||||| ||||| : ||
Db 164 YPSKVNLLSAIKSPCHTESPE 184

RESULT 14

T02558

hypotheical protein At2g32590 [imported] - Arabidopsis thaliana

N:Alternate names: hypotheical protein T26B15.15

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 02-Feb-2001

C:Accession: T02558; A84735

R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes,

submitted to the EMBL Data Library, July 1998

A:Description: Arabidopsis thaliana chromosome II BAC T26B15 genomic sequence.

A:Reference number: Z14678

A:Accession: T02558

A:Status: translated from GB/EMBL/DBBJ

A:Molecule type: DNA

A:Residues: 1-704 <ROU>

A:Cross-references: EMBL:AC004681; NID:g3298532; PID:g3298547

A:Experimental source: cultivar Columbia

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.

cuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: A84735

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-704 <STO>

A:Cross-references: GB:AF002093; NID:g3298547; PIDN:AAC25941.1; GSPDB:GN00139

C:Genetics:

A:Gene: At2g32590; T26B15.15

A:Map position: 2

A:Introns: 89/3; 123/3; 163/1; 184/3; 205/1; 400/3; 449/1; 543/1; 594/3; 631/3

Query Match

Best Local Similarity 40.0%; Score 46; DB 2; Length 704;

Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 4 KVNLLSAIKSPCORETPE 21

| : ||||| : ||

Db 498 KTLPLPASRTPCQTKLPE 515

RESULT 15

B72612

hypotheical protein APE1358 - Aeropyrum pernix (strain K1)

C:Species: Aeropyrum pernix

C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999

C:Accession: B72612

R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah

awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K

DNA Res. 6, 83-101, 1999

A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr

A:Reference number: A72450; MUID:99310339; PMID:10382966

A:Accession: B72612

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-179 <KAW>

A:Cross-references: DDBJ:AP000061; NID:g5104821; PIDN:BAA80352.1; PID:d1044138; PID:g510

A:Experimental source: strain K1

C:Genetics:

A:Gene: APE1358

Query Match

Best Local Similarity 38.3%; Score 44; DB 2; Length 179;

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 4, 2002, 13:18:33 ; Search time 8.68421 Seconds
(without alignments)
105.073 Million cell updates/sec

Title: US-09-754-004-2

Perfect score: 115

Sequence: 1 YOTKVNLLSAIKSPQRETPEG 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	115	100.0	232	1 TNFA_PIG	P23563 sus scrofa
2	115	100.0	233	1 TNFA_CANFA	P51742 canis faml
3	115	100.0	233	1 TNFA_DELE	Q8Wnr1 delphinapte
4	115	100.0	233	1 TNFA_FELCA	P19101 felis silve
5	115	100.0	233	1 TNFA_HUMAN	P01375 homo sapien
6	115	100.0	233	1 TNFA_MACFA	P79337 macaca fasc
7	115	100.0	233	1 TNFA_MACMU	P48094 macaca mula
8	115	100.0	233	1 TNFA_PAPHU	O77510 papio hamad
9	115	100.0	233	1 TNFA_PAPSP	P132620 papio sp. (
10	108	93.9	234	1 TNFA_CAPHI	P13296 capra hircu
11	105	91.3	233	1 TNFA_TURTR	Q9beal turslops tr
12	102	88.7	229	1 TNFA_CEREL	P51743 cervus elap
13	102	88.7	233	1 TNFA_BOVIN	Q06599 bos taurus
14	100	87.0	234	1 TNFA_CAVPO	P51435 cavia porce
15	98	85.2	234	1 TNFA_SHEEP	P23383 ovis aries
16	97	84.3	235	1 TNFA_PERLE	P36939 peromyscus
17	96	83.5	235	1 TNFA_MOUSE	P06804 mus musculu
18	93	80.9	235	1 TNFA_RABIT	P04924 oryctolagus
19	92	80.0	235	1 TNFA_RAT	P16599 rattus norv
20	86	74.8	233	1 TNFA_MARMO	O35734 marmota mon
21	84	73.0	234	1 TNFA_HORSE	P29553 equus cabal
22	80	69.6	233	1 TNFA_MACRU	O77764 macropus eu
23	48	41.7	233	1 TNFA_TRIVU	P79374 trichosurus
24	44	38.3	627	1 Z264_HUMAN	O43296 homo sapien
25	44	38.3	889	1 HFSY_STRPU	Q05068 stronglylce
26	43.5	37.8	329	1 FTSY_BACSU	P51835 bacillus su
27	43	37.4	152	1 Y16D_BPT4	P22917 bacterioph
28	43	37.4	156	1 COAT_RMVCA	Q9wdg7 ribgrass mo
29	43	37.4	156	1 COAT_TVCV	Q88922 turnip vein
30	43	37.4	156	1 RNH_ZYMMV	O69014 zymomonas m
31	42	36.5	156	1 COAT_CRMV	Q66222 chinese rap
32	42	36.5	156	1 COAT_RMV	Q9qee3 ribgrass mo
33	42	36.5	201	1 TNFB_MACEU	Q9xt48 macropus eu

RESULT 1

ID	TNFA_PIG	STANDARD;	PRT;	232 AA.
AC	P23563;			
DT	01-NOV-1991 (Rel. 20, Created)			
DT	01-NOV-1991 (Rel. 20, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor			
DE	ligand superfamily member 2) (Cachectin).			
GN	TNF OR TNESF2 OR TNFA.			
OS	Sus scrofa (Pig).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.			
OX	NCBI_TaxID=9823;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=91016861; PubMed=2216741;			
RA	Drews R.T., Coffee B.W., Prestwood A.K., McGraw R.A.;			
RT	"Gene sequence of porcine tumor necrosis factor alpha.";			
RL	Nucleic Acids Res. 18:5564-5564(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RX	MEDLINE=91340150; PubMed=1874444;			
RA	Kuhnert P., Wuehrich C., Peterhans E., Pauli U.;			
RT	"The porcine tumor necrosis factor-encoding genes: sequence and			
RT	comparative analysis.";			
RL	Gene 102:171-178(1991).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Macrophage;			
RA	Choi C.S., Molitor T.W., Lin G.F., Murtaugh M.P.;			
RT	"Complete nucleotide sequence of a cDNA encoding porcine tumor			
RT	necrosis factor-alpha.";			
RL	Anim. Biotechnol. 2:97-105(1991).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Larqe white; TISSUE=Fibroblast;			
RX	MEDLINE=21108615; PubMed=11169259;			
RA	Chardon P., Rogel-Gaillard C., Cattolico L., Duprat S., Vaiman M.,			
RA	Renard C.;			
RT	"Sequence of the swine major histocompatibility complex region			
RT	containing all non-classical class I genes.";			
RL	Tissue Antigens 57:55-65(2001).			
RN	[5]			
RP	SEQUENCE OF 44-232 FROM N.A.			
RX	MEDLINE=90034181; PubMed=2478420;			
RA	Pauli U., Beutler B., Peterhans E.;			
RT	"Porcine tumor necrosis factor alpha: cloning with the polymerase			
RT	chain reaction and determination of the nucleotide sequence.";			
RL	Gene 81:185-191(1989).			
CC	-!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and			
CC	TNFRSF1B/TNFR2. It is mainly secreted by macrophages and can			
CC	induce cell death of certain tumor cell lines. It is potent			
CC	pyrogen causing fever by direct action or by stimulation of			
CC	interleukin 1 secretion and is implicated in the induction of			

ALIGNMENTS

34	42	36.5	290	1	ARY2_CHICK	P13914
35	42	36.5	458	1	N1FN_AZOVI	gallus gall
36	42	36.5	958	1	BP28_MACFA	azotobacter
37	42	36.5	1224	1	PER_DROME	macaca fasc
38	42	36.5	1400	1	RON_HUMAN	P07663 drosophila
39	42	36.5	2144	1	BP28_HUMAN	Q04912 homo sapien
40	41	35.7	146	1	RNH_AGR15	Q9H583 homo sapien
41	41	35.7	153	1	CORB_MOUSE	Q8Uha7 agrobacteri
42	41	35.7	345	1	VE2_HPV34	Q62267 mus musculu
43	41	35.7	725	1	RRP2_INBSI	P36792 human papil
44	41	35.7	726	1	RRP2_INBAC	P11136 influenza b
45	41	35.7	726	1	RRP2_INBAD	P13874 influenza b

FT CONFLICT 116 116 G -> D (IN REF. 2).
 FT CONFLICT 134 135 IV -> DS (IN REF. 2).
 SQ SEQUENCE 233 AA; 25447 MW; 7B2588FBC8B25340 CRC64;
 Query Match 100.0%; Score 115; DB 1; Length 233;
 Best Local Similarity 100.0%; Pred. No. 2.4e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YQTKVNLSSAIKSPCQRETPG 22
 |||||
 DB 163 YQTKVNLSSAIKSPCQRETPG 184
 |||||
 RESULT 3
 TNFA_DELLE STANDARD; PRT; 233 AA.
 ID Q8WNL1;
 AC 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
 ligand superfamily member 2) (Cachectin).
 GN TNF OR TNFSF2 OR TNFA.
 OS Delphinapterus leucas (Beluga whale).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;
 OC Monodontidae; Delphinapterus.
 OX NCBI_TaxID=9749;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA PubMed=11768130;
 RX Denis F., Archambault D.;
 RT "Molecular cloning and characterization of beluga whale
 (Delphinapterus leucas) interleukin-1beta and tumor necrosis
 factor-alpha.";
 RL Can. J. Vet. Res. 65:233-240(2001).
 CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
 TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
 induce cell death of certain tumor cell lines. It is potent
 pyrogen causing fever by direct action or by stimulation of
 interleukin 1 secretion and is implicated in the induction of
 cachexia, under certain conditions it can stimulate cell
 proliferation and induce cell differentiation (By similarity).
 CC -1- SUBUNIT: Homotrimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
 extracellular soluble form (By similarity).
 CC -1- PPM: The soluble form derives from the membrane form by
 proteolytic processing (By similarity).
 CC -1- PPM: The membrane form, but not the soluble form, is
 phosphorylated on serine residues. Dephosphorylation of the
 membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
 similarity).
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

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 DR EMBL; AF320323; AAL56946.1; .
 DR InterPro: IPR003636; TNF_abc.
 DR InterPro: IPR000478; TNF_family.
 DR Pfam; PF00229; TNF; 1.
 DR PRINTS; PR01234; TNECROSISFCT.
 DR ProDom; PD002012; TNF_abc; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS00251; TNF_1; 1.
 DR PROSITE; PS00049; TNF_2; 1.
 KW Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Phosphorylation;
 Signal-anchor.

FT CHAIN 1 233 TUMOR NECROSIS FACTOR, MEMBRANE FORM.
 FT DOMAIN 78 233 TUMOR NECROSIS FACTOR, SOLUBLE FORM.
 FT TRANSSEM 36 56 CYTOPLASMIC (POTENTIAL).
 FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 (POTENTIAL).
 FT DOMAIN 57 233 EXTRACELLULAR (POTENTIAL).
 FT SITE 77 78 CLEAVAGE (BY ADAM17) (BY SIMILARITY).
 FT MOD_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
 FT DISULFID 145 177 BY SIMILARITY.
 FT CARBOHYD 95 95 N-LINKED (GLCNAC..)(POTENTIAL).
 SQ SEQUENCE 233 AA; 25420 MW; 2DF37DCB2BC9E961 CRC64;
 Query Match 100.0%; Score 115; DB 1; Length 233;
 Best Local Similarity 100.0%; Pred. No. 2.4e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YQTKVNLSSAIKSPCQRETPG 22
 |||||
 DB 163 YQTKVNLSSAIKSPCQRETPG 184
 |||||
 RESULT 4
 TNFA_FELCA STANDARD; PRT; 233 AA.
 ID AC P19101;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
 ligand superfamily member 2) (Cachectin).
 GN TNF OR TNFSF2 OR TNFA.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA PubMed=2216740;
 RX McGraw R.A., Coffee B.W., Otto C.M., Drews R.T., Rawlings C.A.;
 RT "Gene sequence of feline tumor necrosis factor alpha.";
 RL Nucleic Acids Res. 18:5563-5563(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA TISSUP-Bone marrow;
 RA Daniel S.L., Brenner C.A., Legendre A.M., Solomon A., Rouse B.T.;
 RA Submitted (XXX-1993) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
 TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
 induce cell death of certain tumor cell lines. It is potent
 pyrogen causing fever by direct action or by stimulation of
 interleukin 1 secretion and is implicated in the induction of
 cachexia, under certain conditions it can stimulate cell
 proliferation and induce cell differentiation.
 CC -1- SUBUNIT: Homotrimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
 extracellular soluble form (By similarity).
 CC -1- PPM: The soluble form derives from the membrane form by
 proteolytic processing (By similarity).
 CC -1- PPM: The membrane form, but not the soluble form, is
 phosphorylated on serine residues. Dephosphorylation of the
 membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
 similarity).
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

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 DR EMBL; AF320323; AAL56946.1; .
 DR InterPro: IPR003636; TNF_abc.
 DR InterPro: IPR000478; TNF_family.
 DR Pfam; PF00229; TNF; 1.
 DR PRINTS; PR01234; TNECROSISFCT.
 DR ProDom; PD002012; TNF_abc; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS00251; TNF_1; 1.
 DR PROSITE; PS00049; TNF_2; 1.
 KW Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Phosphorylation;
 Signal-anchor.

RA PubMed-10205166;
RA Watts A.D., Hunt N.H., Wanigasekara Y., Bloomfield G., Wallach D.,
RA Roufogalis B.D., Chaudhri G.;
RT "A casein kinase I motif present in the cytoplasmic domain of members
RT of the tumour necrosis factor ligand family is implicated in 'reverse
RT signalling'";
RL EMBO J. 18:2119-2126(1999).
RN [14]
RN MUTAGENESIS.
RX MEDLINE-91184128; PubMed-2009860;
RA Ostade X.V., Tavernier J., Prange T., Fiers W.;
RT "Localization of the active site of human tumour necrosis factor
RT (TNF) by mutational analysis.";
RL EMBO J. 10:827-836(1991).
RN [15]
RN MYRISTOYLATION.
RX MEDLINE-93018820; PubMed-1402651;
RA Stevenson F.T., Bursten S.L., Locksley R.M., Lovett D.H.;
RT "Myristyl acylation of the tumor necrosis factor alpha precursor on
RT specific lysine residues.";
RL J. Exp. Med. 176:1053-1062(1992).
RN [16]
RN CLEAVAGE BY ADAM17.
RX MEDLINE-97186575; PubMed-9034191;
RA Moss M.L., Jin S.-L.C., Milla M.E., Burkhardt W., Carter H.L.,
RA Chen W.-J., Clay W.C., Didsbury J.R., Hassler D., Hoffman C.R.,
RA Kost T.A., Lambert M.H., Leesnitzer M.A., McCauley P., McGeehan G.,
RA Mitchell J., Moyer M., Pabel G., Rocque W., Overton L.K., Schoenen F.,
RA Seton T., Su J.-L., Warner J., Willard D., Becherer J.D.;
RT "Cloning of a disintegrin metalloproteinase that processes precursor
RT tumour-necrosis factor-alpha";
RL Nature 385:733-736(1997).
RN [17]
RN X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX MEDLINE-89159409; PubMed-2922050;
RA Jones E.Y., Stuart D.I., Walker N.P.;
RT "Structure of tumour necrosis factor.";
RL Nature 338:225-228(1989).
RN [18]
RN X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX MEDLINE-91193276; PubMed-1964681;
RA Jones E.Y., Stuart D.I., Walker N.P.;
RT "The structure of tumour necrosis factor -- implications for
RT biological function.";
RL J. Cell Sci. Suppl. 13:11-18(1990).
RN [19]
RN X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RX MEDLINE-90008932; PubMed-2551905;
RA Eck M.J., Sprang S.R.;
RT "The structure of tumor necrosis factor-alpha at 2.6-A resolution.
RT Implications for receptor binding.";
RL J. Biol. Chem. 264:17595-17605(1989).
RN [20]
RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF MUTANT ARG-107.
RX MEDLINE-98147459; PubMed-9488135;
RA Reed C., Fu Z.Q., Wu J., Xue Y.N., Harrison R.W., Chen M.J.,
RA Weber I.T.;
RT "Crystal structure of TNF-alpha mutant R31D with greater affinity for
RT receptor R1 compared with R2";
RL Protein Eng. 10:1101-1107(1997).
RN [21]
RN X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF MUTANT M3S.
RX MEDLINE-98113178; PubMed-9442056;
RA Cha S.S., Kim J.S., Cho H.S., Shin N.K., Jeong W., Shin H.C.,
RA Kim Y.J., Hahn J.H., Oh B.H.;
RT "High resolution crystal structure of a human tumor necrosis factor-
RT alpha mutant with low systemic toxicity.";
RL J. Biol. Chem. 273:2153-2160(1998).
CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
CC induce cell death of certain tumor cell lines. It is potent
CC pyrogen causing fever by direct action or by stimulation of
CC interleukin 1 secretion and is implicated in the induction of
CC cachexia, Under certain conditions it can stimulate cell
CC proliferation and induce cell differentiation.
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC extracellular soluble form (By similarity).
CC -1- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -1- PTM: The membrane form, but not the soluble form, is
CC phosphorylated on serine residues. Dephosphorylation of the
CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC similarity).
CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC AND MALNUTRITION.

CC cachexia, Under certain conditions it can stimulate cell
CC proliferation and induce cell differentiation.
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC EXTRACELLULAR SOLUBLE FORM.
CC -1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
CC PROTEOLYTIC PROCESSING.
CC -1- PTM: The membrane form, but not the soluble form, is
CC phosphorylated on serine residues. Dephosphorylation of the
CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1.
CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC AND MALNUTRITION.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; X02910; CAA26669.1; -.

Query Match 100.0%; Score 115; DB 1; Length 233;
Best Local Similarity 100.0%; Pred. No. 2.4e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YQTKVNLSSAIKSPQRETPEG 22
Db 163 YQTKVNLSSAIKSPQRETPEG 184
|||||

RESULT 6
TNFA_MACFA
ID TNFA_MACFA STANDARD; PRT; 233 AA.
AC P79337;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE ligand superfamily member 2) (Cachectin).
GN TNF OR TNFSF2 OR TNFA.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphocytes;
RA Tatsumi M.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
CC induce cell death of certain tumor cell lines. It is potent
CC pyrogen causing fever by direct action or by stimulation of
CC interleukin 1 secretion and is implicated in the induction of
CC cachexia, Under certain conditions it can stimulate cell
CC proliferation and induce cell differentiation.
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC extracellular soluble form (By similarity).
CC -1- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -1- PTM: The membrane form, but not the soluble form, is
CC phosphorylated on serine residues. Dephosphorylation of the
CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC similarity).
CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC AND MALNUTRITION.

TNFRSF1B/TNFR. It is mainly secreted by macrophages and can induce cell death of certain tumor cell lines. It is potent pyrogen causing fever by direct action or by stimulation of interleukin 1 secretion and is implicated in the induction of cachexia, under certain conditions it can stimulate cell proliferation and induce cell differentiation.

-1- SUBUNIT: Homotrimer (By similarity).

-1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).

-1- PM: The soluble form derives from the membrane form by proteolytic processing (By similarity).

-1- PM: The membrane form, but not the soluble form, is phosphorylated on serine residues. Dephosphorylation of the membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By similarity).

-1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH AND MALNUTRITION.

-1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

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EMBL: AF019963; AAC31675.1; -
 HSP: P01375; 4TSV.
 InterPro: IPR003636; TNF_abc.
 InterPro: IPR000478; TNF_family.
 Pfam: PF00229; TNF; 1.
 PRINTS: PR01234; TNECROSISFCT.
 ProDom: PD02012; TNF_abc; 1.
 SMART: SM00207; TNF; 1.
 PROSITE: PS00251; TNF_1; 1.
 PROSITE: PS50049; TNF_2; 1.
 Cytokine; Cytotoxin; Transmembrane; Phosphorylation; Signal-anchor.
 CHAIN 1 233 TUMOR NECROSIS FACTOR, MEMBRANE FORM.
 SITE 76 77 CLEAVAGE (BY ADAM17) (BY SIMILARITY).
 MOD_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
 DISULFID 145 177 BY SIMILARITY.
 SEQUENCE 233 AA; 25658 MW; B9403255058D4A03 CRC64;

Query Match 100.0%; Score 115; DB 1; Length 233;
 Best Local Similarity 100.0%; Pred. No. 2.4e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YQTKVNLLSAIKSPCQRETPG 22
 |||||
 Db 163 YQTKVNLLSAIKSPCQRETPG 184

RESULT 9
 TNFA_PAPSP STANDARD; PRT; 233 AA.
 AC P33620;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor ligand superfamily member 2) (Cachectin).
 GN TNF OR TNFSF2 OR TNFA.
 OS Papio sp. (Baboon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Papio.

NCBI_TaxID=61183;
 [1]
 SEQUENCE FROM N.A.
 RA Sanjanwala M., Edwards A.;
 RL Submitted (SEP-1991) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
 TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
 CC induce cell death of certain tumor cell lines. It is potent
 CC pyrogen causing fever by direct action or by stimulation of
 CC interleukin 1 secretion and is implicated in the induction of
 CC cachexia, under certain conditions it can stimulate cell
 CC proliferation and induce cell differentiation.
 CC -1- SUBUNIT: Homotrimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
 CC extracellular soluble form (By similarity).
 CC -1- PM: The soluble form derives from the membrane form by
 CC proteolytic processing (By similarity).
 CC -1- PM: The membrane form, but not the soluble form, is
 CC phosphorylated on serine residues. Dephosphorylation of the
 CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
 CC similarity).
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

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EMBL: X62141; CAA44068.1; -
 PIR: S22052; S22052.
 HSP: P01375; IA8M.
 InterPro: IPR003636; TNF_abc.
 InterPro: IPR000478; TNF_family.
 Pfam: PF00229; TNF; 1.
 PRINTS: PR01234; TNECROSISFCT.
 ProDom: PD02012; TNF_abc; 1.
 SMART: SM00207; TNF; 1.
 PROSITE: PS00251; TNF_1; 1.
 PROSITE: PS50049; TNF_2; 1.
 Cytokine; Cytotoxin; Transmembrane; Phosphorylation; Signal-anchor.
 CHAIN 1 233 TUMOR NECROSIS FACTOR, MEMBRANE FORM.
 SITE 76 77 TUMOR NECROSIS FACTOR, SOLUBLE FORM.
 DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).
 TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).
 DOMAIN 57 233 EXTRACELLULAR (POTENTIAL).
 SITE 76 77 CLEAVAGE (BY ADAM17) (BY SIMILARITY).
 MOD_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
 LIPID 19 19 MYRISTATE (BY SIMILARITY).
 LIPID 20 20 MYRISTATE (BY SIMILARITY).
 DISULFID 145 177 BY SIMILARITY.
 SEQUENCE 233 AA; 25557 MW; 455360B48DC74173 CRC64;

Query Match 100.0%; Score 115; DB 1; Length 233;
 Best Local Similarity 100.0%; Pred. No. 2.4e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YQTKVNLLSAIKSPCQRETPG 22
 |||||
 Db 163 YQTKVNLLSAIKSPCQRETPG 184

RESULT 10
 TNFA_CAPHI STANDARD; PRT; 234 AA.
 ID TNFA_CAPHI
 AC P13296; Q28320; Q9MYF2;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)

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CC DR EMBL; AB049358; BAB39855.1; -.
CC DR HSSP; P01375; 4TSV.
CC DR InterPro; IPR003636; TNF_abc.
CC DR InterPro; IPR000478; TNF_family.
CC DR Pfam; PF00229; TNF; 1.
CC DR PRINTS; PR01234; TNECROSISFCT.
CC DR ProDom; PD002012; TNF_abc; 1.
CC DR SMART; SM00207; TNF; 1.
CC DR PROSITE; PS00251; TNF_1; 1.
CC DR PROSITE; PS50049; TNF_2; 1.
CC DR Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Phosphorylation;
CC Signal-anchor.
CC FT CHAIN 1 233 TUMOR NECROSIS FACTOR, MEMBRANE FORM.
CC FT CHAIN 78 233 TUMOR NECROSIS FACTOR, SOLUBLE FORM.
CC FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
CC FT (POTENTIAL).
CC FT DOMAIN 57 233 EXTRACELLULAR (POTENTIAL).
CC FT SITE 77 78 CLEAVAGE (BY ADAM17) (BY SIMILARITY).
CC FT MOD_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
CC FT DISULFID 145 177 BY SIMILARITY.
CC FT CARBOHYD 95 95 N-LINKED (GLCNAC...) (POTENTIAL).
CC FT SEQUENCE 233 AA; 25404 MW; 71CC39C699CC49D9 CRC64;

Query Match 91.3%; Score 105; DB 1; Length 233;
Best Local Similarity 90.9%; Pred. No. 9.8e-10;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YQTKVNLISAISKPCQRETPG 22
| : ||||| ||||| ||||| |||||
Db 163 YPSKVNLISAISKPCQRETPG 184

RESULT 12
TNFA_CEREL ID TNFA_CEREL STANDARD; PRT; 229 AA.
AC P51743;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
GN TNF OR TNFSF2 OR TNFA.
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=9860;
RN [1]
RP SEQUENCE FROM N.A.
RA Lockhart E.A.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC TNFRSF1B/TNFR2. It is mainly secreted by macrophages and can
CC induce cell death of certain tumor cell lines. It is potent
CC pyrogen causing fever by direct action or by stimulation of
CC interleukin 1 secretion and is implicated in the induction of
CC cachexia. Under certain conditions it can stimulate cell
CC proliferation and induce cell differentiation.
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).
CC -1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
CC PROTEOLYTIC PROCESSING (BY SIMILARITY).
CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC AND MALNUTRITION.

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CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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EMBL; U14683; AAA50759.1; -.
HSSP; P01375; 4TSV.
InterPro; IPR003636; TNF_abc.
InterPro; IPR000478; TNF_family.
Pfam; PF00229; TNF; 1.
ProDom; PD002012; TNF_abc; 1.
SMART; SM00207; TNF; 1.
PROSITE; PS00251; TNF_1; 1.
PROSITE; PS50049; TNF_2; 1.
Cytokine; Cytotoxin; Transmembrane; Signal-anchor.
NON_TER 1 1 TUMOR NECROSIS FACTOR, MEMBRANE FORM.
CHAIN <1 229 TUMOR NECROSIS FACTOR, SOLUBLE FORM.
CHAIN 74 229 CYTOPLASMIC (POTENTIAL).
DOMAIN <1 30 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
TRANSMEM 31 51 (POTENTIAL).
DOMAIN 52 229 EXTRACELLULAR (POTENTIAL).
SITE 72 73 CLEAVAGE (BY ADAM17) (BY SIMILARITY).
DISULFID 141 173 BY SIMILARITY.
SEQUENCE 229 AA; 24987 MW; 16DES3F7AA5A7DB35 CRC64;

Query Match 88.7%; Score 102; DB 1; Length 229;
Best Local Similarity 90.5%; Pred. No. 3e-09;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YQTKVNLISAISKPCQRETPG 21
| : ||||| ||||| |||||
Db 159 YQTKVNLISAISKPCQRETPG 179

RESULT 13
TNFA_BOVIN ID TNFA_BOVIN STANDARD; PRT; 233 AA.
AC Q06599; O18779;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
GN TNF OR TNFSF2 OR TNFA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94083525; PubMed=8260599;
RA Cludts I., Cleuter Y., Kettmann R., Burny A., Droogmans L.;
RT "Cloning and characterization of the tandemly arranged bovine
RT lymphotoxin and tumour necrosis factor-alpha genes.";
RL Cytokine 5:336-341(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Boran, and N'Dama;
RA Iraqi F.;
RT "Bovine TNF-alpha gene.";
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 50-233 FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=9600582; PubMed=7590981;
RA Mertens B.E.L.C., Muriuki M., Gaidullis L.;


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RT Cloning of two members of the TNF-superfamily in cattle: CD40 ligand
RL Immunogenetics 42:430-431(1995).
CC -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC induce cell death of certain tumor cell lines. It is potent
CC pyrogen causing fever by direct action or by stimulation of
CC interleukin 1 secretion and is implicated in the induction of
CC cachexia. Under certain conditions it can stimulate cell
CC proliferation and induce cell differentiation.
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC extracellular soluble form (By similarity).
CC -!- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -!- PTM: The membrane form, but not the soluble form, is
CC phosphorylated on serine residues. Dephosphorylation of the
CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC similarity).
CC -!- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC AND MALNUTRITION.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC
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CC
DR EMBL; Z14137; CAA78511.1; -.
DR EMBL; AF011926; AAB84086.1; -.
DR EMBL; AF011927; AAB84087.1; -.
DR EMBL; Z48808; CAA88743.1; -.
DR PIR; S24642; S24642.
DR HSSP; P01375; 4TSV.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
KW Cytokine; Cytotoxin; Transmembrane; Phosphorylation; Signal-anchor;
KW Polymorphism.
FT CHAIN 1 233 TUMOR NECROSIS FACTOR, MEMBRANE FORM.
FT CHAIN 78 233 TUMOR NECROSIS FACTOR, SOLUBLE FORM.
FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT DOMAIN 57 233 EXTRACELLULAR (POTENTIAL).
FT SITE 77 78 CLEAVAGE (BY ADAM17) (BY SIMILARITY).
FT MOD_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
FT DISULFID 145 177 BY SIMILARITY.
FT VARIANT 48 48 F -> C (IN STRAIN N'DAMA).
FT CONFLICT 62 62 E -> EQ (IN REF. 3).
FT SEQUENCE 233 AA; 25439 MW; 8AF55C002A9763B0 CRC64;
Query Match 88.7%; Score 102; DB 1; Length 233;
Best Local Similarity 90.5%; Pred. No. 3e-09;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 YQKVNLLSAIKSPCHRETP 21
| | | | | : | | | | | | | | | |
Db 163 YQKVNLLSAIKSPCHRETP 183
*RESULT 14
TNFA_CAVPO STANDARD; PRT; 234 AA.
ID . TNFA_CAVPO

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AC P51435;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE ligand superfamily member 2) (Cachectin).
GN TNF OR TNFSF2 OR TNFA.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=Hartley; TISSUE=Lung;
RA Yuan H.T., Kelly F.J., Bingle C.D.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RP STRAIN=Dunkin-Hartley;
RA White A.M., Yoshimura T., Smith A.W., Westwick J., Watson M.L.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RT "Airway inflammation induced by recombinant guinea pig tumor necrosis
RT factor-alpha."; 273:1524-1530(1997).
RL CC
CC -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
CC induce cell death of certain tumor cell lines. It is potent
CC pyrogen causing fever by direct action or by stimulation of
CC interleukin 1 secretion and is implicated in the induction of
CC cachexia. Under certain conditions it can stimulate cell
CC proliferation and induce cell differentiation.
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC extracellular soluble form (By similarity).
CC -!- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -!- PTM: The membrane form, but not the soluble form, is
CC phosphorylated on serine residues. Dephosphorylation of the
CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC similarity).
CC -!- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC AND MALNUTRITION.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC
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CC
DR EMBL; U39839; AAB06492.1; -.
DR EMBL; U77036; AAB19210.1; -.
DR HSSP; P06804; 2TNF.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
KW Cytokine; Cytotoxin; Transmembrane; Phosphorylation; Signal-anchor.
FT CHAIN 1 234 TUMOR NECROSIS FACTOR, MEMBRANE FORM.
FT CHAIN 80 234 TUMOR NECROSIS FACTOR, SOLUBLE FORM.
FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT DOMAIN 57 234 EXTRACELLULAR (POTENTIAL).
FT SITE 79 80 CLEAVAGE (BY ADAM17) (BY SIMILARITY).
FT MOD_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).

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FT DISULFID 147 178 BY SIMILARITY..
SQ SEQUENCE 234 AA; 25793 MW; 7272C940393E7E9B CRC64;

Query Match 87.0%; Score 100; DB 1; Length 234;
Best Local Similarity 86.4%; Pred. No. 6.4e-09;
Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YQTKVNLLSAIKSPCQRETPEG 22
Db 164 YPERVNLLSAIKSPCQRETPEG 185

RESULT 15
TNFA_SHEEP STANDARD; PRT; 234 AA.
AC P23383;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE ligand superfamily member 2) (Cachectin).
-GN TNF OR TNFSF2 OR TNFA.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA MEDLINE=91067496; PubMed=2251151;
RA Young A.J., Hay J.B., Chan J.Y.C.;
RT "Primary structure of ovine tumor necrosis factor alpha cDNA.";
RL Nucleic Acids Res. 18:6723-6723(1990).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Alveolar macrophage;
RX MEDLINE=92112044; PubMed=1765267;
RA Green I.R., Sargan D.R.;
RT "Sequence of the cDNA encoding ovine tumor necrosis factor-alpha:
RT problems with cloning by inverse PCR.";
RL Gene 109:203-210(1991).
[3]
RP SEQUENCE FROM N.A.
RX MEDLINE=92155784; PubMed=1786996;
RA Andrews A.E., Nash A.D., Barcham G.J., Brandon M.R.;
RT "Molecular cloning, expression and characterization of ovine TNF
RT alpha.";
RL Immunol. Cell Biol. 69:273-283(1991).
CC -I- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
CC induce cell death of certain tumor cell lines. It is potent
CC pyrogen causing fever by direct action or by stimulation of
CC interleukin 1 secretion and is implicated in the induction of
CC cachexia. Under certain conditions it can stimulate cell
CC proliferation and induce cell differentiation.
CC -I- SUBUNIT: Homotrimer (By similarity).
CC -I- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC extracellular soluble form (By similarity).
CC -I- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -I- PTM: The membrane form, but not the soluble form, is
CC phosphorylated on serine residues. Dephosphorylation of the
CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC similarity).
CC -I- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC AND MALNUTRITION.
CC -I- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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CC the European Bioinformatics Institute. There are no restrictions on its
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CC -----
DR EMBL; X55966; CAA39437.1; -;
DR EMBL; X55152; CAA38952.1; -;
DR EMBL; X56756; CAA40076.1; -;
DR EMBL; A19163; CAA01445.1; -;
DR PIR; S13114; S13114;
DR PIR; S20661; S20661;
DR PIR; JH0529; JH0529;
DR HSSP; P01375; 4TSV.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF.1; 1.
DR PROSITE; PS00049; TNF.2; 1.
KW Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Phosphorylation;
KW Signal-anchor.
FT CHAIN 1 234 TUMOR NECROSIS FACTOR, MEMBRANE FORM.
FT CHAIN 78 234 TUMOR NECROSIS FACTOR, SOLUBLE FORM.
FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT DOMAIN 57 234 (POTENTIAL).
FT SITE 77 78 EXTRACELLULAR (POTENTIAL).
FT MOD_RES 2 2 CLEAVAGE (BY ADAM17) (BY SIMILARITY).
FT DISULFID 146 178 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
FT CARBOHYD 96 96 BY SIMILARITY.
FT CONFLICT 63 63 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 234 AA; 25536 MW; 4BCF8CCAB7956B88 CRC64;

Query Match 85.2%; Score 98; DB 1; Length 234;
Best Local Similarity 86.4%; Pred. No. 1.3e-08;
Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YQTKVNLLSAIKSPCQRETPEG 22
Db 164 YQTKVNLLSAIKSPCHRETELEG 185

Search completed: December 4, 2002, 13:23:02
Job time : 9.68421 secs
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 4, 2002, 13:20:58 ; Search time 28.9474 Seconds
(without alignments)
156.596 Million cell updates/sec

Title: US-09-754-004-2

Perfect score: 115

Sequence: 1 YOTKVNLLSAIKSPCQRETPEG 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phase.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_rvirus.*

16: sp_bacteriap.*

17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	115	100.0	66	4 Q9P1Q2	Q9P1Q2 homo sapien
2	115	100.0	149	6 Q97543	Q97543 actus nancy
3	115	100.0	217	6 Q9BEG1	Q9BEG1 bradypus tr
4	115	100.0	217	6 Q9BEG0	Q9BEG0 cyclopes di
5	115	100.0	217	6 Q9BEF4	Q9BEF4 cabassous u
6	115	100.0	232	4 Q9UIV3	Q9UIV3 homo sapien
7	110	95.7	157	4 Q43647	Q43647 homo sapien
8	105	91.3	138	6 Q9TTG7	Q9TTG7 actus lemur
9	105	91.3	149	6 Q97538	Q97538 actus vocif
10	105	91.3	149	6 Q97TC8	Q97TC8 actus nigri
11	102	88.7	104	6 Q27978	Q27978 bos taurus
12	102	88.7	217	6 Q9BEC5	Q9BEC5 tenrec ecau
13	101	87.8	216	6 Q9BEE9	Q9BEE9 ochotona pr
14	97	84.3	215	6 Q9BEE8	Q9BEE8 erinaceus e
15	97	84.3	217	11 Q9ERG6	Q9ERG6 peromyscus
16	95	82.6	216	6 Q9BEC4	Q9BEC4 talpa europ

17	94	81.7	156	11	Q91ZL4	Q91ZL4 sigmodon hi
18	92	80.0	216	11	O70332	O70332 mesocricetu
19	92	80.0	235	11	Q9J127	Q9J127 rattus norv
20	92	80.0	235	11	Q9J126	Q9J126 rattus norv
21	86	74.8	215	11	Q99ND1	Q99ND1 tamiascluru
22	80	69.6	216	6	Q9BEE0	Q9BEE0 macropus ru
23	72	62.6	214	6	Q9BEF3	Q9BEF3 didelphis m
24	65	56.5	234	6	Q9TTJ3	Q9TTJ3 equus cabal
25	57	49.6	99	6	Q95LE8	Q95LE8 canis famil
26	49	42.6	225	13	Q91B42	Q91B42 paralichthy
27	49	42.6	225	13	Q91B41	Q91B41 paralichthy
28	48	41.7	65	6	Q95N81	Q95N81 canis famil
29	46	40.0	704	10	O80896	O80896 arabisdopsis
30	46	40.0	4167	5	Q9GPN8	Q9GPN8 drosophila
31	45	39.1	175	4	O8VWH1	O8VWH1 homo sapien
32	45	39.1	245	11	Q8R217	Q8R217 mus musculu
33	45	39.1	632	5	Q8T095	Q8T095 drosophila
34	45	39.1	942	6	Q9BDV4	Q9BDV4 equus cabal
35	44.5	38.7	961	10	Q9FS96	Q9FS96 saccharum o
36	44	38.3	108	11	Q9CRL4	Q9CRL4 mus musculu
37	44	38.3	179	17	Q9YC96	Q9YC96 aeropyrum p
38	44	38.3	251	10	Q9FXJ6	Q9FXJ6 arabidopsis
39	44	38.3	396	10	Q9AW63	Q9AW63 guillaroia
40	44	38.3	543	5	Q9V852	Q9V852 drosophila
41	44	38.3	889	5	Q94769	Q94769 strongyloce
42	44	38.3	959	2	O87815	O87815 alcaligenes
43	44	38.3	1208	5	Q9U4W1	Q9U4W1 aedes aegyp
44	43.5	37.8	230	5	O16265	O16265 caenorhabdi
45	43	37.4	129	12	Q86705	Q86705 tobamovirus

ALIGNMENTS

RESULT 1

ID	Q9P1Q2	PRELIMINARY;	PRT;	66 AA.
AC	Q9P1Q2:			
DT	01-OCT-2000 (TREMBlrel. 15, Created)			
DT	01-OCT-2000 (TREMBlrel. 15, Last sequence update)			
DT	01-DEC-2001 (TREMBlrel. 19, Last annotation update)			
DE	APC1 protein (Fragment).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=PROSTATE TUMOR;			
RA	Shao C., Yan W., Zhu F., Yue W., Chai Y., Zhao Z., Wang C.;			
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF098751; AAF11992.1; -			
DR	HSSP; P01375; 57SW.			
DR	InterPro; IPR003636; TNF_abc.			
DR	InterPro; IPR000478; TNF_family.			
DR	Pfam; PF00229; TNF; 1.			
DR	PRINTS; PR01234; TNECROSISFCT.			
DR	PRODOM; PD002012; TNF_abc; 1.			
DR	PROSITE; PS50049; TNF_2; 1.			
FT	NON_TER 66			
SQ	SEQUENCE 66 AA; 7300 MW; C58DC35377E6D368 CRC64;			

Query Match 100.0%; Score 115; DB 4; Length 66;
Best Local Similarity 100.0%; Pred. No. 1.6e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YOTKVNLLSAIKSPCQRETPEG 22

Db 15 YOTKVNLLSAIKSPCQRETPEG 36

RESULT 2

Q97543

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Query Match          100.0%; Score 115; DB 6; Length 217;
Best Local Similarity 100.0%; Pred. No. 5.5e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY      1  YQTKVNLLSAIKSPCQRETPEG 22
          |||||
Db       155 YQTKVNLLSAIKSPCQRETPEG 176

RESULT 4
Q9BEGO
ID      Q9BEGO      PRELIMINARY;      PRT;      217 AA.
AC      Q9BEGO;
DT      01-JUN-2001 (T-EMBLrel. 17, Created)
DT      01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT      01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DE      Tumor necrosis factor (Fragment).
GN      TNFA.
OS      Cyclopes didactylus (silky anteater).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Edentata; Myrmecophagidae; Cyclopes.
OX      NCBI_TaxId=84074;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      van Dijk M.A.M.; de Jong W.W.;
RT      "Indels indicate that rodents are monophyletic and lagomorphs are
RT      their sister group.";
RL      Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RR      EMBL; AJ286828; CAC28514.1; -.
RR      HSSP; P01375; 1A8M.
DR      InterPro; IPR003636; TNF_abc.
DR      InterPro; IPR000478; TNF_family.
DR      Pfam; PF00229; TNF; 1.
DR      PRINTS; PR01234; TNCRGOSISFCT.
DR      ProDom; PD002012; TNF_abc; 1.
DR      SMART; SM00207; TNF; 1.
DR      PROSITE; PS00251; TNF_1; 1.
DR      PROSITE; PS50049; TNF_2; 1.

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SQ      SEQUENCE      217 AA;  23753 MW;   F760E887F6C29EBB CRC64;

Query Match          100.0%; Score 115; DB 6; Length 217;
Best Local Similarity 100.0%; Pred. No. 5.5e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YQTKVNLLSAIKSPCORETPEG 22
        |||||
Db       155 YQTKVNLLSAIKSPCORETPEG 176

RESULT 5
Q9BEF4 PRELIMINARY; PRT; 217 AA.
ID      Q9BEF4 AC
DT      01-JUN-2001 (TrEMBLrel. 17, Created)
DI      01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT      01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE      Tumor necrosis factor (Fragment).
GN      TNFA.
OS      Cabassous unicinctus (Southern naked-tailed armadillo).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Edentata; Dasypodidae; Cabassous.
NCBI_TaxID=48852;
[1]
RN      RP
RP      SEQUENCE FROM N.A.
RA      van Dijk M.A.M., de Jong W.W.;
RT      *Indels indicate that rodents are monophyletic and lagomorphs are
RT      their sister group.*;
RL      Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AJ286829; CAB28518.1; -.
DR      HSPSP; P01375; 4TSV.
DR      InterPro: IPR003636; TNF abc.

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DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF_1; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER 1
FT NON_TER 217
SQ SEQUENCE 217 AA; 23742 MW; 83C591DD6883FD86 CRC64;

Query Match 100.0%; Score 115; DB 6; Length 217;
Best Local Similarity 100.0%; Pred. No. 5.9e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YOTKVNLLSAIKSPCQRETPG 22
Db 155 YOTKVNLLSAIKSPCQRETPG 176
|||||
RESULT 6
Q9UIV3 PRELIMINARY; PRT; 232 AA.
ID Q9UIV3
AC Q9UIV3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Tumor necrosis factor.
GN TNF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93272029; PubMed=8499947;
RA Iris F., Bougueleret L., Prieur S., Caterina D., Primas G., Perrot V.,
RA Jurka J., Rodriguez-Tome P., Claverie J., Cohen D., Dausset J.;
RT "Dense Alu clustering and a potential new member of the NFKappaB
RT family within a 90 kilobase HLA class III segment.";
RL Nat. Genet. 3:137-145(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96215741; PubMed=8629302;
RA Utans U., Quist W.C., McManus B.M., Wilson J.E., Arcenci R.J.,
RA Wallace A.F., Russell M.E.;
RT "Allograft inflammatory factory-1. A cytokine-responsive macrophage
RT molecule expressed in transplanted human hearts.";
RL Transplantation 61:1387-1392(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=96006565; PubMed=7590964;
RA Holzinger I., de Baey A., Messer G., Kick G., Zwierzina H.,
RA Weiss E.H.;
RT "Cloning and genomic characterization of LST1: a new gene in the human
RT TNF region.";
RL Immunogenetics 42:315-322(1995).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=93208881; PubMed=7916655;
RA Browning J.L., Ngam-ek A., Lawton P., DeMarinis J., Tizard R.,
RA Chow E.P., Hession C., O'Brine-Greco B., Foley S.F., Ware C.F.;
RT "Lymphotoxin-beta: A new member of the TNF family that forms a
RT heteromeric complex with lymphotoxin on the cell surface.";
RL Cell 72:847-856(1993).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=86016093; PubMed=2995927;
RA Nedwin G.E., Naylor S.L., Sakaguchi A.Y., Smith D., Jarrett-Nedwin J.,
RA Pennica D., Goeddel D.V., Gray P.W.;
RT "Human lymphotoxin and tumor necrosis factor genes: structure,
RT homology and chromosomal localization.";
RL Nucleic Acids Res. 13:6361-6373(1985).

[6]
RN SEQUENCE FROM N.A.
RX MEDLINE=91086846; PubMed=1670638;
RA Messer G., Spengler U., Jung M.C., Honold G., Bloemer K., Pape G.R.,
RA Riethmuller G., Weiss E.H.;
RT "Polymorphic Structure of the Tumor Necrosis Factor (TNF) Locus: An
RT Ncol Polymorphism in the First Intron of the Human TNF-beta Gene
RT Correlates with A Variant Amino Acid in Position 26 and a Reduced
RT Level of TNF-beta Production.";
RL J. Exp. Med. 173:209-219(1991).
RN [7]
RN SEQUENCE FROM N.A.
RX MEDLINE=91139175; PubMed=1671667;
RA Abraham L.J., Du D.C., Zahedi K., Dawkins R.L., Whitehead A.S.;
RA "Haplotypic polymorphisms of the TNFB gene.";
RL Immunogenetics 33:50-53(1991).
RN [8]
RN SEQUENCE FROM N.A.
RX MEDLINE=94362679; PubMed=8081366;
RA Albertella M.R., Campbell D.R.;
RT "Characterization of a novel gene in the human major
RT histocompatibility complex that encodes a potential new member of the
RT I kappa B family of proteins.";
RL Hum. Mol. Genet. 3:793-799(1994).
RN [9]
RN SEQUENCE FROM N.A.
RX MEDLINE=95324911; PubMed=7601445;
RA Peelman L., Chardon P., Nunes M., Renard C., Geffrotin C., Valman M.,
RA Van Zeveren J., Coppieters W., Van de Weghe A., Bouquet Y., Choy W.,
RA Strominger J., Spies T.;
RT "The BAT1 Gene in the MHC Encodes an Evolutionarily Conserved Putative
RT Nuclear RNA Helicase of the D-E-A-D Family.";
RL Genomics 26:210-218(1995).
RN [10]
RN SEQUENCE FROM N.A.
RX MEDLINE=20132445; PubMed=10668961;
RA Neville M.J., Campbell R.D.;
RT "Alternative splicing of the LST-1 gene located in the major
RT histocompatibility complex on human chromosome 6.";
RL DNA Seq. 8:155-160(1997).
RN [11]
RN SEQUENCE FROM N.A.
RX MEDLINE=98035883; PubMed=9367684;
RA de Baey A., Fellerhoff B., Maier S., Martinozzi S., Weidle U.,
RA Weiss E.H.;
RT "Complex expression pattern of the TNF region gene LST1 through
RT differential regulation, initiation, and alternative splicing.";
RL Genomics 45:591-600(1997).
RN [12]
RN SEQUENCE FROM N.A.
RX MEDLINE=98145985; PubMed=9480751;
RA Shina T., Tamiya G., Oka A., Yamagata T., Yamagata N., Kikkawa E.,
RA Goto K., Mizuki N., Watanabe K., Fukuzumi Y., Taguchi S., Sugawara C.,
RA Ogo A., Chen L., Yamazaki M., Tashiro H., Ando A., Ikemura T.,
RA Kimura M., Inoko H.;
RT "Nucleotide sequencing analysis of the 146-kilobase segment around the
RT IKBL and MICA genes at the centromeric end of the HLA Class I
RL region.";
RL Genomics 47:372-382(1998).
DR EMBL; Y14768; CAA75070.1; -.
DR HSSP; P01375; 4TSV.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
SQ SEQUENCE 232 AA; 25446 MW; E4D71B19C6AE0D03 CRC64;

Query Match 100.0%; Score 115; DB 4; Length 232;
Best Local Similarity 100.0%; Pred. No. 5.9e-12;

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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YQTKVNLLSAIKSPCQRETPG 22
DB 162 YQTKVNLLSAIKSPCQRETPG 183

RESULT 7
O43647 PRELIMINARY; PRT; 157 AA.
AC O43647;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Tumor necrosis factor alpha (Fragment).
GN TNFA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Jang J.S., Kim B.E.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF043342; AAC03542.1; -.
DR HSSP; P01375; 1A8M.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER 1
SQ SEQUENCE 157 AA; 17380 MW; D1344822267E9F20 CRC64;

Query Match 95.7%; Score 110; DB 4; Length 157;
Best Local Similarity 95.5%; Pred. No. 2.9e-11;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YQTKVNLLSAIKSPCQRETPG 22
DB 87 YQTKVNLLSAIKSPCQRETPG 108

RESULT 8
Q9TTG7 PRELIMINARY; PRT; 138 AA.
AC Q9TTG7;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
DE Tumor necrosis factor alpha (Fragment).
GN TNF-ALPHA.
OS Aotus lemurinus (Northern gray-necked night monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=43147;
RN [1]
RP SEQUENCE FROM N.A.
RA Murillo L.A., Hernandez E., Echeverry S.J., Mendez J.A.,
RA Patarroyo M.E.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF09329; AAF21304.1; -.
DR HSSP; P01375; 4TSV.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF; 1.

DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER 1
SQ SEQUENCE 149 AA; 16415 MW; 86F1B9BCED16E689 CRC64;

Query Match 91.3%; Score 105; DB 6; Length 149;
Best Local Similarity 90.9%; Pred. No. 2.1e-10;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YQTKVNLLSAIKSPCQRETPG 22
DB 80 YQTKVNLLSAIKSPCQRETPG 101

RESULT 10
Q9TTG8 PRELIMINARY; PRT; 149 AA.
AC Q9TTG8;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Tumor necrosis factor alpha (Fragment).
GN TNF-ALPHA.
OS Aotus nigripes (black-headed night monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=57175;
RN [1]
RP SEQUENCE FROM N.A.
RA Murillo L.A., Hernandez E., Echeverry S.J., Mendez J.A.,
RA Patarroyo M.E.;

DR PRINTS; PR01234; TNECROSISFCT.
DR PRODOM; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS0049; TNF_2; 1.
FT NON_TER 1
FT NON_TER 217
SQ SEQUENCE 217 AA; 23964 MW; D6F90C74C0B3021F CRC64;

Query Match 84.3%; Score 97; DB 11; Length 217;
Best Local Similarity 81.8%; Pred. No. 8e-09; Indels 0; Gaps 0;
Matches 18; Conservative 2; Mismatches 2;

Qy 1 YQTKVNLLSAIKSPCQRETPEG 22
I: |||||:|||||:|||||
Db 157 YEDKVNLLSAIKSPCQRETPEG 178

Search completed: December 4, 2002, 13:24:00
Job time : 29.9474 secs

QY 1 YQTKVNLLSAIKSPCQRETPEG 22
I: |||||:|||||:|||||
DB 154 YPNKVNLLSAIKSPCQKETPEG 175

RESULT 14
Q9BEE8 PRELIMINARY; PRT; 215 AA.
AC Q9BEE8;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Tumor necrosis factor (Fragment).
GN TNFA.
OS Erinaceus europaeus (Western European hedgehog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceinae; Erinaceus.
OX NCBI_TaxID=9365;
RN [1]
RP SEQUENCE FROM N.A.
RA van Dijk M.A.M., de Jong W.W.;
RT "Indels indicate that rodents are monophyletic and lagomorphs are their sister group."
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ286830; CAC28522.1; -
DR HSP; P01375; 4TSV.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR PRODOM; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS0049; TNF_2; 1.
FT NON_TER 1
FT NON_TER 215
SQ SEQUENCE 215 AA; 23696 MW; 3E337E7E65F074EA CRC64;

Query Match 84.3%; Score 97; DB 6; Length 215;
Best Local Similarity 86.4%; Pred. No. 7.9e-09; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 3;

QY 1 YQTKVNLLSAIKSPCQRETPEG 22
I: |||||:|||||:|||||
DB 153 YQKDVNLLSAIKSPCQSETPEG 174

RESULT 15
Q9ERG6 PRELIMINARY; PRT; 217 AA.
AC Q9ERG6;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Tumor necrosis factor alpha (Fragment).
OS Peromyscus maniculatus (Deer mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Peromyscus.
OX NCBI_TaxID=10042;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN;
RA Herbst M.M., Schountz T.;
RT "Cloning of the deer mouse interferon gamma, interleukin-10 and tumor necrosis factor genes."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307013; AAG30264.1; -
DR HSP; P06804; 2TNF.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
FT NON_TER 1
FT NON_TER 217

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 4, 2002, 13:18:13 ; Search time 35.8947 Seconds
(without alignments)
81.670 Million cell updates/sec

Title: US-09-754-004-2

Perfect score: 115

Sequence: 1 YQTKVNLSSAIKSPCQRETPEG 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002.*

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- 13: /SID22/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
- 14: /SID22/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
- 15: /SID22/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
- 16: /SID22/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
- 17: /SID22/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
- 18: /SID22/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
- 19: /SID22/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SID22/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SID22/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	115	100.0	22	AAW22950	htNF-alpha epitope
2	115	100.0	22	AAW59149	Human tumour necro
3	115	100.0	140	AAW72456	Tumour necrosis fa
4	115	100.0	145	9 AAP82043	Sequence of new tu
5	115	100.0	147	9 AAP81853	Sequence of modifi
6	115	100.0	147	22 AAB67245	Human tumour necro
7	115	100.0	147	22 AAB71982	C-terminal region
8	115	100.0	149	10 AAF91635	Polypeptide derive
9	115	100.0	149	11 AAR05612	Antitumour peptide
10	115	100.0	150	8 AAP70528	Synthetic tumour n

11	115	100.0	150	8 AAP71245	TNF-derived polype
12	115	100.0	150	9 AAP81236	Modified tumour ne
13	115	100.0	150	9 AAP81066	Sequence of new ph
14	115	100.0	150	9 AAP81088	Sequence of new ph
15	115	100.0	150	10 AAP95660	Anti-tumour active
16	115	100.0	150	11 AAR05286	New polypeptide wi
17	115	100.0	150	11 AAR08151	Polypeptide with a
18	115	100.0	150	12 AAR11011	TNF-like polypepti
19	115	100.0	150	12 AAR11723	Tumour Necrosis Fa
20	115	100.0	150	13 AAR29808	TNF analogue #1.
21	115	100.0	150	13 AAR29809	TNF analogue #2.
22	115	100.0	150	15 AAR69579	Human TNF mutein.
23	115	100.0	150	15 AAR69580	Human TNF mutein.
24	115	100.0	150	15 AAR69581	Human TNF mutein.
25	115	100.0	150	15 AAR69582	Human TNF mutein.
26	115	100.0	151	9 AAP81251	Tumoricide polypep
27	115	100.0	151	9 AAP81233	Anti-tumour peptid
28	115	100.0	151	10 AAP93187	Sequence of modifi
29	115	100.0	151	11 AAR05865	Polypeptide with a
30	115	100.0	151	11 AAR07900	Anti-tumour peptid
31	115	100.0	151	11 AAR07900	Antitumour polypep
32	115	100.0	151	12 AAR11615	Tumour Necrosis Fa
33	115	100.0	151	12 AAR11703	Tumour Necrosis Fa
34	115	100.0	151	12 AAR11613	Tumour Necrosis Fa
35	115	100.0	151	12 AAR11714	Tumour necrosis fa
36	115	100.0	151	12 AAR11860	Truncated Tumour N
37	115	100.0	151	12 AAR11861	Improved Tumour N
38	115	100.0	151	12 AAR11753	Tumour Necrosis Fa
39	115	100.0	151	12 AAR11967	Human TNF with mod
40	115	100.0	151	12 AAR11968	Tumour Necrosis Fa
41	115	100.0	151	12 AAR11969	Truncated human TN
42	115	100.0	151	12 AAR13816	TNF analogue encod
43	115	100.0	151	12 AAR14305	TNF analogue encod
44	115	100.0	151	12 AAR14687	Human tumour necro
45	115	100.0	152	9 AAP81239	Anti-tumour polype

ALIGNMENTS

RESULT 1	
AAW22950	
ID	AAW22950 standard; peptide: 22 AA.
XX	
AC	AAW22950;
XX	
DT	05-MAR-1998 (first entry)
XX	
DE	htNF-alpha epitope 87-108.
XX	
KW	tumour necrosis factor alpha; TNF; epitope: antibody; antagonist;
KW	fibrinogen; cardiovascular; cerebrovascular; thrombosis; stroke;
KW	thrombophlebitis; myocardial infarction; embolism; ischaemia.
XX	
OS	Homo sapiens.
XX	
PN	WO9730088-A2.
XX	
PD	21-AUG-1997.
XX	
PF	17-FEB-1997; 97WO-GB00435.
XX	
PR	16-FEB-1996; 96US-0602272.
XX	
PA	(KENN-) KENNEDY INST RHEUMATOLOGY.
XX	
PI	Elliott MJH, Feldmann M, Maini RN;
XX	
DR	WPI; 1997-424980/39.
XX	
PT	Treating and preventing cardiovascular, cerebrovascular or
PT	thrombotic disorder, or decreasing plasma fibrinogen - by
PT	administration of tumour necrosis factor antagonist

XX Claim 10; Page 14; 57pp; English.

XX The invention relates to the use of an antagonist of tumour necrosis

CC factor (TNF) for the treatment of vascular disease, cardiovascular

CC disorders, thrombotic disorders, or illnesses or pathologies which

CC are treatable by decreasing plasma fibrinogen. Typical conditions which

CC can be treated include acute myocardial infarction, deep vein thrombosis,

CC thrombophlebitis, stroke, thromboembolic disorder or ischemic events.

CC In one embodiment the antagonist used is an anti-TNF antibody

CC (optionally chimeric, humanised or resurfaced), preferably one which

CC binds to an epitope comprising at least 5 amino acids within the region

CC TNF-alpha 87-108 and/or TNF-alpha 59-80. The present sequence represents

CC the 87-108 epitope.

XX Sequence 22 AA;

Query Match 100.0%; Score 115; DB 18; Length 22;

Best Local Similarity 100.0%; Pred. No. 4.1e-12;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YQTKVNLISAIKSPCQRTPEG 22

Db 1 YQTKVNLISAIKSPCQRTPEG 22

RESULT 2

AAW59149

ID AAW59149 standard; peptide; 22 AA.

XX AAW59149;

XX 13-AUG-1998 (first entry)

XX Human tumour necrosis factor-alpha epitope pos. 87-108.

XX Tumour necrosis factor-alpha; epitope; human immunodeficiency virus;

KW HIV; TNF-alpha; anti-TNF; antibody; treatment; prevention; infection;

KW acquired immune deficiency disease; interleukin-2; IL-2; gene therapy;

KW systemic toxicity; CD4+ cell; inflammation; immune response.

XX Homo sapiens.

XX WO9811917-A1.

XX 26-MAR-1998.

XX 17-SEP-1997; 97WO-US16116.

XX 19-SEP-1996; 96US-0716107.

XX (CENZ) CENTOCOR INC.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX McCloskey RV, Walker RE, Woody JN;

XX WPI; 1998-230303/20.

XX Treating or preventing acquired immune deficiency syndrome using

PT interleukin-2 - and antibodies against tumour necrosis factor, to

PT reduce side effects of the treatment

XX Claim 10; Page 11; 50pp; English.

XX This peptide sequence is a fragment of tumour necrosis factor-alpha

CC (TNF-alpha) corresponding to amino acid position 87-108 of the full

CC length protein. This region is an epitope and is recognized and/or binds

CC with anti-TNF activity. This fragment is used to describe a novel method

CC of treating or preventing acquired immune deficiency disease and

CC infection with human immune deficiency virus (HIV) by co-administration

CC of interleukin-2 (IL-2) and a chimeric antibody (Ab), or its fragment,

CC against tumour necrosis factor (TNF). IL-2 and Ab are administered by

CC injection, orally, topically or are produced from gene therapy vectors,

CC but preferably by intravenous injection or infusion. Usual doses are

CC 0.01-100 (especially 1-40) mg/kg/day, in 1-6 portions or in sustained

CC release form. Further doses may be given, just before or during relapse.

CC Inhibition of TNF alpha by Ab alleviates some of the systemic toxicity

CC associated with administration of IL-2 (which increases the level of CD4+

CC cells but also stimulates production of TNF, high levels of which cause

CC unwanted inflammatory and immunological responses). Blockade of TNF

CC allows administration of higher doses of IL-2 than would be otherwise

CC possible.

XX Sequence 22 AA;

Query Match 100.0%; Score 115; DB 19; Length 22;

Best Local Similarity 100.0%; Pred. No. 4.1e-12;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YQTKVNLISAIKSPCQRTPEG 22

Db 1 YQTKVNLISAIKSPCQRTPEG 22

RESULT 3

AAR72456

ID AAR72456 standard; protein; 140 AA.

XX AAR72456;

XX 19-DEC-1995 (first entry)

XX Tumour necrosis factor-alpha 4th exon fragment.

XX Tumour necrosis factor; fusion protein; metastasis; inhibition.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "This residue has the peptide AAR72454

FT attached at the N-terminus"

XX TW239078-A.

XX 21-JAN-1995.

XX 12-OCT-1993; 93TW-0108498.

XX 29-SEP-1993; 93JP-0020556.

XX (MIZU/) MIZUNO D.

PA (SONA/) SONAMOTO I.

XX Sonamoto I;

XX WPI; 1995-168947/22.

XX Pharmaceutical and veterinary composition for inhibiting metastasis

PT - can be made into tablet form

XX Disclosure; Page 5; 14pp; Chinese.

XX The amino acid sequence of a part of the 4th exon from the tumour

CC necrosis factor (TNF)-alpha. The protein has the peptide AAR72454

CC attached to the N-terminal amino acid. The fusion protein can be

CC used in pharmaceutical compositions for inhibiting metastasis.

XX Sequence 140 AA;

Query Match 100.0%; Score 115; DB 16; Length 140;

Best Local Similarity 100.0%; Pred. No. 3.5e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YQTKVNLISAIKSPCQRTPEG 22

|||||

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Db      70 YQTKVNLLSAIKSPCQRETPEG 91
RESULT 4
AAP82043
ID    AAP82043 standard; protein; 145 AA.
XX
XX    AAP82043;
XX
XX    12-DEC-1990 (first entry)
XX
XX    Sequence of new tumour necrosis factor (TNF).
XX
XX    Anticancer drug; lymphokine; antitumour.
XX
XX    Homo sapiens.
XX
XX    JP63032486-A.
XX
XX    12-FEB-1988.
XX
XX    25-JUL-1986; 86JP-0173822.
XX
XX    25-JUL-1986; 86JP-0173822.
XX
XX    (TEIJ ) TEIJIN KK.
XX
XX    WPI; 1988-080331/12.
XX
XX    New biologically active polypeptide - useful as anticancer agent
XX
XX    Claim 2(1); Page 547; 17pp; Japanese.
XX
XX    New biologically active polypeptide has cytotoxic activity specifically
XX    for tumour cells and, therefore, is expected to be used as an anticancer
XX    drug. It is derived from human TNF by deleting 11 N-terminal AAs. (See
XX    also J63188396, AAN81624 and AAP81236).
XX
XX    Sequence 145 AA;
XX
XX    Query Match 100.0%; Score 115; DB 9; Length 145;
XX    Best Local Similarity 100.0%; Pred. No. 3.7e-11;
XX    Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX    1 YQTKVNLLSAIKSPCQRETPEG 22
XX    |||||
XX    76 YQTKVNLLSAIKSPCQRETPEG 97
XX
RESULT 5
AAP81853
ID    AAP81853 standard; protein; 147 AA.
XX
XX    AAP81853;
XX
XX    17-DEC-1990 (first entry)
XX
XX    Sequence of modified human tumour necrosis factor (hTNF).
XX
XX    Antitumour; anticancer; cytostatic.
XX
XX    Homo sapiens.
XX
XX    JP62272991-A.
XX
XX    27-NOV-1987.
XX
XX    21-MAY-1986; 86JP-0114754.
XX
XX    21-MAY-1986; 86JP-0114754.
XX
XX    (TEIJ ) TEIJIN KK.
XX
DR      WPI; 1988-010365/02.
DR      N-PSDB; AAN82306.
XX
XX    New bioactive polypeptide -
XX    has antitumour activity, and is obtd. by culturing bacteria
XX    transformed with plasmid contg. DNA sequence of the polypeptide
XX
XX    Claim 2(1); Page 761; 20pp; Japanese.
XX
XX    DNA sequence encoding hTNF was synthesised chemically and inserted into
XX    vector plasmid. Recombinant plasmid was cut with restriction enzyme and
XX    DNA fragment coding for new bioactive polypeptide was obtd. The new
XX    bioactive polypeptide has ten N-terminal AAs deleted. It has antitumour
XX    activity greater than hTNF and can be produced by culturing bacteria
XX    transformed with a plasmid contg. DNA encoding the polypeptide.
XX
XX    Sequence 147 AA;
XX
XX    Query Match 100.0%; Score 115; DB 9; Length 147;
XX    Best Local Similarity 100.0%; Pred. No. 3.7e-11;
XX    Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX    1 YQTKVNLLSAIKSPCQRETPEG 22
XX    |||||
XX    77 YQTKVNLLSAIKSPCQRETPEG 98
XX
RESULT 6
AAB67245
ID    AAB67245 standard; protein; 147 AA.
XX
XX    AAB67245;
XX
XX    18-APR-2001 (first entry)
XX
XX    Human tumour necrosis factor alpha.
XX
XX    Human; Apo2 ligand; divalent metal ions; viral infection; cancer.
XX
XX    Homo sapiens.
XX
XX    WO200100832-A1.
XX
XX    04-JAN-2001.
XX
XX    26-JUN-2000; 2000WO-US17579.
XX
XX    28-JUN-1999; 99US-0141342.
XX
XX    (GETH ) GENENTECH INC.
XX
XX    Ashkenazi AJ, Hymowitz S, Kelley RF, Koumenis I, Leung S;
XX    O'Connell M, Pai R, Shahrokh Z, Simmons L;
XX
XX    WPI; 2001-123012/13.
XX
XX    Use of divalent metal ions for making Apo-2 ligand and in formulations
XX    containing Apo-2 ligand for increasing yield and stability of ligand
XX    trimers, useful for therapeutic applications -
XX
XX    Disclosure; Fig 3; 60pp; English.
XX
XX    The present invention relates to a formulation comprising Apo-2
XX    ligand and divalent metal ions. Apo-2 ligand and the formulation
XX    are useful for treating cancers and viral infections. Addition
XX    of divalent metal ions for making Apo-2 ligand and formulations
XX    containing Apo-2 ligand results in increased yield and stability
XX    of Apo-2 ligand trimers.
XX
XX    Sequence 147 AA;
XX
XX    Query Match 100.0%; Score 115; DB 22; Length 147;
XX    Best Local Similarity 100.0%; Pred. No. 3.7e-11;

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Db      79 YQTKVNLLSAIKSPCQRETPEG 100
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RESULT 9
AAR05612
ID      AAR05612 standard; protein; 149 AA.
XX      AC
XX      AAR05612;
XX      DT 29-OCT-1990 (first entry)
XX      DE Antitumour peptide.
XX      KW Antitumour; cancer; tumour necrosis factor; ds.
XX      OS Synthetic.
XX      PN JP02128696-A.
XX      PD 17-MAY-1990.
XX      PF 09-NOV-1988; 88JP-0281364.
XX      PR 09-NOV-1988; 88JP-0281364.
XX      PA (TEIJ ) TEIJIN KK.
XX      WPI; 1990-196692/26.
XX      N-PSDB; AAQ05036.
XX      New physiologically active polypeptide -
PT      contains specific amino acid sequence, shows antitumour effect
PT      and has low side effect.
XX      PS Disclosure; : 18pp; Japanese.
XX      CC DNA is synthesised from 17 oligonucleotides TNF-1 to TNF-17.
CC      The gene product may be truncated by 12 N-terminal AAs, and
CC      residue Leu-157 may be replaced by Phe
XX      XX
SQ      Sequence 149 AA;
Query Match 100.0%; Score 115; DB 11; Length 149;
Best Local Similarity 100.0%; Pred. NO. 3.8e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YQTKVNLLSAIKSPCQRETPEG 22
Db      80 YQTKVNLLSAIKSPCQRETPEG 101
|||||
RESULT 10
AAR70528
ID      AAR70528 standard; protein; 150 AA.
XX      AC
XX      AAR70528;
XX      DT 30-JAN-1991 (first entry)
XX      DE Synthetic tumour necrosis factor mutant.
XX      KW Tumour necrosis factor; mutant; antitumour agent; vector pTNF 416;
XX      PN JP62248498-A.
XX      PD 29-OCT-1987.
XX      PF 21-APR-1986; 86JP-0090087.
XX      PR 21-APR-1986; 86JP-0090087.
XX      PA (TEIJ ) TEIJIN KK.
```

```
XX      WPI; 1987-345004/49.
DR      N-PSDB; AAN70852.
XX      New bioactive polypeptide - having antitumour activity and higher
PT      activity than human tumour necrosis factor.
XX      PS Claim 1; page 623; 18pp; Japanese.
XX      CC The mutant of tumour necrosis factor (TNF) is constructed by
CC      modifying the sequence of human TNF and deleting 7 N-terminal amino
CC      acids. The mutant has activity 2.8 times that of human TNF.
CC      It is expressed using expression vector pTNF 416 in E.coli.
CC      The cells are then cultured to give the mutant in an amt. of 15.5%
CC      of total proteins. The antitumour activity of this protein was
CC      measured using mouse L-929 fibroblast cells. 100 microlitres of
CC      E.coli lysate contg. 0.00006 units had specific activity of the
CC      mutant of 0.0000088 units/mg.
XX      SQ Sequence 150 AA;
Query Match 100.0%; Score 115; DB 8; Length 150;
Best Local Similarity 100.0%; Pred. NO. 3.8e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YQTKVNLLSAIKSPCQRETPEG 22
Db      80 YQTKVNLLSAIKSPCQRETPEG 101
|||||
RESULT 11
AAP71245
ID      AAP71245 standard; Protein; 150 AA.
XX      AC AAP71245;
XX      DT 29-APR-1991 (first entry)
XX      DE TNF-derived polypeptide.
XX      KW Tumour necrosis factor.
XX      OS Homo sapiens.
XX      PN JP62091198-A.
XX      PD 25-APR-1987.
XX      PF 26-FEB-1986; 86JP-0040733.
XX      PR 21-JUN-1985; 85JP-0136280.
XX      PR 26-FEB-1985; 85EP-0102093.
XX      PR 23-APR-1985; 85JP-0087297.
XX      PR 26-FEB-1986; 86JP-0040733.
XX      PA (DAIN ) DAINIPPON PHARM KK.
XX      WPI; 1987-153959/22.
DR      N-PSDB; AAN71245.
XX      Tumoricidal polypeptide(s) - are prepd. by cleaving specified DNA
PT      with pertinent restriction enzyme(s) and bonding with
PT      conventional synthetic DNA adaptor.
XX      PS Claim 1; Page 1; 20pp; Japanese.
XX      CC The polypeptide was obtd. by cleaving DNA encoding mature TNF. The
CC      resulting fragment was then ligated to a synthetic DNA adapter and
CC      inserted into an expression vector for prodn. of the polypeptide
CC      which has tumoricidal activity. The N-terminal may have up to three
CC      residues deleted resulting in N-terminals of: Met-Ser-Asp-Lys,
CC      Met-Asp-Lys, or Met-Lys.
XX      XX
```

```
SQ Sequence 150 AA;
Query Match 100.0%; Score 115; DB 8; Length 150;
Best Local Similarity 100.0%; Pred. No. 3.8e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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   |||||
Db 80 YQTKVNLLSAIKSPCQRETPEG 101

RESULT 12
AAP81236
ID AAP81236 standard; protein; 150 AA.
XX
AC AAP81236;
XX
DT 15-OCT-1990 (first entry)
XX
DE Modified tumour necrosis factor.
XX
KW Tumour necrosis factor; cytotoxic agent; antitumour drug; cancer.
XX
OS Synthetic.
XX
PN JP63188396-A.
XX
PD 03-AUG-1988.
XX
PF 30-JAN-1987; 87JP-0018566.
XX
PR 30-JAN-1987; 87JP-0018566.
XX
PA (TEIJ ) TEIJIN KK.
XX
WPI; 1988-260396/37.
DR N-PSDB; AAN81624.
XX
New biologically active polypeptide - is modified tumour necrosis
PT factor with cytotoxic activity to cancer cells.
XX
PS Claim 1; Page 1; 20pp; Japanese.
XX
CC A DNA sequence produced from synthetic oligonucleotides can be
used, in an expression vector, to produce the recombinant polypeptide
CC which has a broad action spectrum and causes few side effects.
XX
SQ Sequence 150 AA;
Query Match 100.0%; Score 115; DB 9; Length 150;
Best Local Similarity 100.0%; Pred. No. 3.8e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 80 YQTKVNLLSAIKSPCQRETPEG 101

RESULT 13
AAP81066
ID AAP81066 standard; protein; 150 AA.
XX
AC AAP81066;
XX
DT 14-SEP-1990* (first entry)
XX
DE Sequence of new physiologically active polypeptide with antitumour
DE activity.
XX
KW Antitumour; Escherichia coli.
XX
PN JP63226298-A.
XX
```

```
PD 20-SEP-1988.
XX
XX 16-MAR-1987; 87JP-0059007.
XX
PR 16-MAR-1987; 87JP-0059007.
XX
PA (TEIJ ) TEIJIN KK.
XX
WPI; 1988-305170/43.
DR P-PSDB; AAP81066.
XX
New physiologically active polypeptide used as antitumour agent -
PT obtd. by culturing recombinant Escherichia coli cell transformed by
PT plasmid contg. DNA region coding the polypeptide
XX
PS Claim 2 (4); Page 670; 20pp; Japanese.
XX
CC A recombinant microorganism cell transformed by recombinant plasmid
CC contg. the DNA region coding for the polypeptide is cultured. The
CC polypeptide is isolated from the resulting culture. The microorganism
CC is pref. Escherichia coli.
XX
SQ Sequence 150 AA;
Query Match 100.0%; Score 115; DB 9; Length 150;
Best Local Similarity 100.0%; Pred. No. 3.8e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YQTKVNLLSAIKSPCQRETPEG 22
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Db 80 YQTKVNLLSAIKSPCQRETPEG 101

RESULT 14
AAP81068
ID AAP81068 standard; protein; 150 AA.
XX
AC AAP81068;
XX
DT 14-SEP-1990 (first entry)
XX
DE Sequence of new physiologically active polypeptide with antitumour
DE activity.
XX
KW Antitumour; Escherichia coli.
XX
PH Key Location/Qualifiers
FT Misc-difference 1 /label=OTHER
FT /note="NH2-Arg"
FT Misc-difference 150 /label=OTHER
FT /note="Leu-COOH"
XX
PN JP63226297-A.
XX
PD 20-SEP-1988.
XX
XX 16-MAR-1987; 87JP-0059006.
XX
PR 16-MAR-1987; 87JP-0059006.
XX
PA (TEIJ ) TEIJIN KK.
XX
WPI; 1988-305169/43.
DR N-PSDB; AAN81497.
XX
New physiologically active anti tumour polypeptide -
PT pred. by culturing recombinant microorganism cell transformed by
PT recombinant plasmid contg. DNA coding polypeptide
XX
PS Claim 2 (1); Page 669; 20pp; Japanese.
XX
```

CC A recombinant microorganism cell transformed by recombinant plasmid
CC contg. the DNA region coding for the polypeptide is cultured. The
CC polypeptide is isolated from the resulting culture. The microorganism
CC is pref. Escherichia coli.
XX

SQ Sequence 150 AA;

Query Match 100.0%; Score 115; DB 9; Length 150;
Best Local Similarity 100.0%; Pred. NO. 3.8e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|
Db 80 YQTKVNLLSAIKSPCQRETPG 101

RESULT 15

AAP95660
ID AAP95660 standard; protein; 150 AA.

XX

AC AAP95660;

XX

DT 14-AUG-1989 (first entry)

XX

DE Anti-tumour active polypeptide.

XX

KW Antitumour drug; human tumour necrosis factor.

XX

OS Synthetic.

XX

PN JF01165400-A.

XX

PD 29-JUN-1989.

XX

PF 22-DEC-1987; 87JP-0322838.

XX

PR 22-DEC-1987; 87JP-0322838.

XX

PA (TEIJ) TEIJIN KK.

XX

DR WPI; 1989-230773/32.

XX

PT New biologically active polypeptide - useful as antitumour drug.

XX

PS Disclosure; fig 1; 23pp; Japanese.

XX

CC This sequence is derived from the human tumour necrosis factor amino acid
CC sequence. A region corresp. to the N-terminal 11 residues of the natural
CC seq. is deleted and repair synthesis using the AA sequence: Arg-Lys-Arg
CC is carried out. Fig. 1 is amended to produce the new sequence.
CC Resultant polypeptide has an increased antitumour activity (1.6 x 100,
CC 000 000) compared with human TNF (2.3 x 10,000 000).

SQ Sequence 150 AA;

Query Match 100.0%; Score 115; DB 10; Length 150;
Best Local Similarity 100.0%; Pred. NO. 3.8e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 80 YQTKVNLLSAIKSPCQRETPG 101

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Job time : 35.8947 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 4, 2002, 13:24:03 ; Search time 8.10526 Seconds
(without alignments)
44.086 Million cell updates/sec

Title: us-09-754-004-2

Perfect score: 115

Sequence: 1 YQTKVNLISAQSPQRETPG 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 103943 seqs, 16242309 residues

Total number of hits satisfying chosen parameters: 103943

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	115	100.0	22	8	US-08-602-272-2
2	115	100.0	22	10	US-09-754-004-2
3	115	100.0	150	10	US-09-877-156-25
4	115	100.0	150	12	US-10-116-378-28
5	115	100.0	152	9	US-09-779-050A-24
6	115	100.0	157	9	US-09-903-327A-7
7	115	100.0	157	10	US-09-756-301A-1
8	115	100.0	157	10	US-09-927-703-1
9	115	100.0	157	10	US-09-854-280-19
10	115	100.0	157	10	US-09-934-465-13
11	115	100.0	157	10	US-09-766-535A-1
12	115	100.0	157	10	US-09-854-208-19
13	115	100.0	157	10	US-09-756-161A-1
14	115	100.0	157	12	US-10-010-229-1
15	115	100.0	157	12	US-10-043-450-1
16	115	100.0	157	12	US-10-044-534-1
17	115	100.0	164	10	US-09-798-789-2
18	115	100.0	164	10	US-09-981-289-2
19	115	100.0	193	9	US-10-145-014-3

Sequence 3, Appli
Sequence 5, Appli
Sequence 3, Appli
Sequence 22, Appli
Sequence 5, Appli
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Sequence 43, Appli
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Sequence 5, Appli
Sequence 10, Appli
Sequence 11, Appli
Sequence 40, Appli
Sequence 8, Appli
Sequence 7, Appli
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Sequence 14, Appli
Sequence 37065, A
Sequence 4992, Ap
Sequence 10904, A
Sequence 942, App
Sequence 496, App
Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-602-272-2
; Sequence 2, Application US/08602272
; Patent No. US20020081306A1
; GENERAL INFORMATION:
; APPLICANT: Elliott, Michael J.
; APPLICANT: Maini, Ravinder N.
; APPLICANT: Feldmann, Marc
; TITLE OF INVENTION: Methods of Preventing or Treating
; TITLE OF INVENTION: Cardiovascular, Cerebrovascular and Thrombotic Disorders
; TITLE OF INVENTION: with Tumor Necrosis Factor Antagonists
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173-4799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,272
; FILING DATE:
; CLASSIFICATION: 504
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: KIR96-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-9540
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-602-272-2

Query Match 100.0%; Score 115; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.9e-12;
Matches 22: Conservative 0; Mismatches 0 Indels

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Db 1 YQTKVNLLSAIKSPCQRETPEG 22
|||||

RESULT 2

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US-09-754-004-2
; Sequence 2, Application US/09754004
; Patent No. US20020010180A1
; GENERAL INFORMATION:
; APPLICANT: Marc Feldmann
; APPLICANT: Ravinder N. Maini
; TITLE OF INVENTION: TNF Alpha Antagonists and Methotrexate
; TITLE OF INVENTION: in the Treatment of TNF-Mediated Disease
; FILE REFERENCE: 2891.1001-026
; CURRENT APPLICATION NUMBER: US/09/754,004
; CURRENT FILING DATE: 2001-01-03
; PRIOR APPLICATION NUMBER: 08/690,775
; PRIOR FILING DATE: 1996-08-01
; PRIOR APPLICATION NUMBER: 08/607,419
; PRIOR FILING DATE: 1996-02-28
; PRIOR APPLICATION NUMBER: PCT/GB94/00462
; PRIOR FILING DATE: 1994-03-10
; PRIOR APPLICATION NUMBER: PCT/GB93/02070
; PRIOR FILING DATE: 1993-10-06
; PRIOR APPLICATION NUMBER: 07/958,248
; PRIOR FILING DATE: 1992-10-08
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-754-004-2

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Query Match 100.0%; Score 115; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.9e-12;
Matches 22; Conservative 0; Mismatches 0; Indels

QY 1 YQTKVNLLSAIKSPCQRETPEG 22
|||||

Dh 1 YQTKVNLLSAIKSPCQRETPEG 22
|||||

RESULT 3

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US-09-877-156-25
; Sequence 25, Application US/09877156
; Patent No. US20020055625A1
; GENERAL INFORMATION:
; APPLICANT: Cathener Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/877,156
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/286,529
; PRIOR FILING DATE: 1998-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 150
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-877-156-25

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Query Match	100.0%;	Score 115;	DB 10;	Length 150;
Best Local Similarity	100.0%;	Pred. No., 1.7e-11;		
Matches 22:	Conservative	0;	Mismatches 0;	Indels 0;
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db 80 YOTKVNLLSAIKSPCQRETPEG 101

RESULT 4

US-10-116-378-28

Sequence 28, Application US/10116378
Patent No. US20020150993A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin
APPLICANT: Marsters, Scott A.
APPLICANT: Pitti, Robert M.
APPLICANT: Wood, William
TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND
TITLE OF INVENTION: NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P1206R1
CURRENT APPLICATION NUMBER: US/10/116, 378
CURRENT FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/247, 225
PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/074, 087
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09
NUMBER OF SEQ ID NOS: 31
SEQ ID NO 28
LENGTH: 150
TYPE: PRT
ORGANISM: Homo sapiens
US-10-116-378-28

Query Match 100.0%; Score 115; DB 12; Length 150;
Best Local Similarity 100.0%; Pred. No. 1.7e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      80 YQTKVNLLSAIKSPCQRETPEG 101
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RESULT, T 5

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US-09-779-050A-24
; Sequence 24, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSD, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Homo sapiens
; SS-09-779-050A-24

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Db 87 YOTKVNLLSAIKSPCQRETPEG 108

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US-09-854-280-19
; Sequence 19, Application US/09854280
; Patent No. US20020052027A1

; GENERAL INFORMATION:

; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Wood, William I.

; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF

; FILE REFERENCE: P1381R12
; CURRENT APPLICATION NUMBER: US/09/854,280
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/311,832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/085,579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 60/113,621
; PRIOR FILING DATE: 1998-12-23

; NUMBER OF SEQ ID NOS: 26

; SEQ ID NO 19
; LENGTH: 157

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-854-280-19

Query Match 100.0%; Score 115; DB 10; Length 157;

Best Local Similarity 100.0%; Pred. No. 1.8e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YOTKVNLLSAIKSPCQRETPEG 22

|||||

Db 87 YOTKVNLLSAIKSPCQRETPEG 108

RESULT 10

US-09-934-465-13
; Sequence 13, Application US/09934465
; Patent No. US2002010233A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: APO-2 LIGAND
; FILE REFERENCE: 11669.22US03
; CURRENT APPLICATION NUMBER: US/09/934,465
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 08/584,031
; PRIOR FILING DATE: 1996-01-09

; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 13

; LENGTH: 157

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-934-465-13

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Best Local Similarity 100.0%; Pred. No. 1.8e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 87 YOTKVNLLSAIKSPCQRETPEG 108

RESULT 11

US-09-766-535A-1
; Sequence 1, Application US/09766535A
; Patent No. US20020106372A1

; GENERAL INFORMATION:
; APPLICANT: Le, Junning
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Ghayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; TITLE OF INVENTION: Human Tumor Necrosis Factor
; FILE REFERENCE: 0975.1005-010
; CURRENT APPLICATION NUMBER: US/09/766,535A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
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; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; PRIOR FILING DATE: 1991-03-18
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-766-535A-1

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Best Local Similarity 100.0%; Pred. No. 1.8e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-09-854-208-19
; Sequence 19, Application US/09854208
; Patent No. US20020106743A1

; GENERAL INFORMATION:

; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES
; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: P1381-R1
; CURRENT APPLICATION NUMBER: US/09/854,208
; CURRENT FILING DATE: 2001-05-10

; PRIOR APPLICATION NUMBER: US/09/311,832

; PRIOR FILING DATE: 1999-05-14

; PRIOR APPLICATION NUMBER: US 60/085,579

; PRIOR FILING DATE: 1998-05-15

; PRIOR APPLICATION NUMBER: US 60/113,621

; PRIOR FILING DATE: 1998-12-23

RESULT 14
US-10-010-229-1

; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; PRIOR FILING DATE: 1991-03-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-043-450-1

Query Match 100.0%; Score 115; DB 12; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.8e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
Db 87 YOTKVNLLSAIKSPCQRETPEG 108
|||||

Search completed: December 4, 2002, 13:30:35
Job time : 9.10526 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 4, 2002, 13:21:18 ; Search time 13.3158 Seconds
(without alignments)
48.612 Million cell updates/sec

Title: US-09-754-004-2

Perfect score: 115

Sequence: 1 YQTKVLLSAIKSPCQRETPEG 22

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Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
 - 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
 - 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
 - 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
 - 5: /cgn2_6/ptodata/1/iaa/PCRU_COMB.pep.*
 - 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	115	100.0	22	4	US-08-690-775-2
2	115	100.0	147	1	US-07-668-517-1
3	115	100.0	147	4	US-09-105-343A-9
4	115	100.0	148	1	US-07-668-517-2
5	115	100.0	148	1	US-07-668-517-15
6	115	100.0	149	1	US-07-668-517-3
7	115	100.0	149	1	US-07-668-517-16
8	115	100.0	150	1	US-07-668-517-4
9	115	100.0	150	1	US-07-668-517-5
10	115	100.0	150	1	US-07-668-517-6
11	115	100.0	150	1	US-07-668-517-8
12	115	100.0	150	1	US-07-668-517-9
13	115	100.0	150	1	US-07-668-517-10
14	115	100.0	150	1	US-07-668-517-11
15	115	100.0	150	1	US-07-668-517-12
16	115	100.0	150	1	US-07-668-517-13
17	115	100.0	150	1	US-07-668-517-14
18	115	100.0	150	1	US-07-668-517-17
19	115	100.0	150	1	US-07-668-517-29
20	115	100.0	150	1	US-07-668-517-31
21	115	100.0	150	1	US-07-668-517-35
22	115	100.0	150	1	US-07-668-517-37
23	115	100.0	150	1	US-07-994-469A-6
24	115	100.0	150	1	US-07-994-469A-7
25	115	100.0	150	1	US-07-994-469A-8
26	115	100.0	150	1	US-07-994-469A-57
27	115	100.0	150	4	US-09-286-529-25

28 115 100.0 151 1 US-07-668-517-7 Sequence 7, Appl
29 115 100.0 151 1 US-07-668-517-18 Sequence 18, Appl
30 115 100.0 151 1 US-07-668-517-19 Sequence 19, Appl
31 115 100.0 151 1 US-07-668-517-20 Sequence 20, Appl
32 115 100.0 151 1 US-07-668-517-22 Sequence 22, Appl
33 115 100.0 151 1 US-07-668-517-23 Sequence 23, Appl
34 115 100.0 151 1 US-07-668-517-24 Sequence 24, Appl
35 115 100.0 151 1 US-07-668-517-25 Sequence 25, Appl
36 115 100.0 151 1 US-07-668-517-26 Sequence 26, Appl
37 115 100.0 151 1 US-07-668-517-27 Sequence 27, Appl
38 115 100.0 151 1 US-07-668-517-28 Sequence 28, Appl
39 115 100.0 151 1 US-07-668-517-30 Sequence 30, Appl
40 115 100.0 151 1 US-07-668-517-32 Sequence 32, Appl
41 115 100.0 151 1 US-07-668-517-36 Sequence 36, Appl
42 115 100.0 151 1 US-07-668-517-38 Sequence 38, Appl
43 115 100.0 152 1 US-07-668-517-21 Sequence 21, Appl
44 115 100.0 155 1 US-07-763-512-1 Sequence 1, Appl
45 115 100.0 155 1 US-07-994-469A-1 Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-690-775-2
; Sequence 2, Application US/08690775
; Patent No. 6270766
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Marc
; APPLICANT: Maini, Ravinder N.
; TITLE OF INVENTION: ANTI-TNF ANTIBODIES AND METHOTREXATE IN
; TITLE OF INVENTION: THE TREATMENT OF AUTOIMMUNE DISEASE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: TWO MILITIA DRIVE
; CITY: LEXINGTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/690,775
; FILING DATE: 01-AUG-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/607,419
; FILING DATE: 28-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB94/00462
; FILING DATE: 15-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/02070
; FILING DATE: 06-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/958,248
; FILING DATE: 08-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook Esq., David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: KIR92-01A4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS:

TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-690-775-2

Query Match 100.0%; Score 115; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 6.8e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YQTKVNLSSAISKPCQRETPEG 22
Db 1 YQTKVNLSSAISKPCQRETPEG 22

RESULT 2

US-07-668-517-1
Sequence 1, Application US/07668517
Patent No. 5262309

GENERAL INFORMATION:

APPLICANT: SATOSHI NAKAMURA et al.
TITLE OF INVENTION: No. 5262309el Physiologically Active
TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism
TITLE OF INVENTION: Cell, Pharmaceutical Composition and Method of Recovering
NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/668,517

FILING DATE: 19910322

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Matthew Jacob

REGISTRATION NUMBER: 25,154

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-8850

TELEFAX: 202-371-8856

TELEX:

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 147 amino acids

TYPE: AMINO ACID

STRANDEDNESS: single

TOPOLOGY: linear

FEATURE:

NAME/KEY:

LOCATION:

IDENTIFICATION METHOD:

OTHER INFORMATION:

US-07-668-517-1

Query Match 100.0%; Score 115; DB 1; Length 147;
Best Local Similarity 100.0%; Pred. No. 6.2e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YQTKVNLSSAISKPCQRETPEG 22
Db 77 YQTKVNLSSAISKPCQRETPEG 98

RESULT 3

US-09-105-343A-9
Sequence 9, Application US/09105343A
Patent No. 6207642
GENERAL INFORMATION:
APPLICANT: WILEY, S.R.
TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL
TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-6050
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FASTSEQ For Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,343A
FILING DATE: 12-FEB-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/02859
FILING DATE: 12-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: BECKER, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6048 US.P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-935-1729
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 147 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6207642e
US-09-105-343A-9

Query Match 100.0%; Score 115; DB 4; Length 147;
Best Local Similarity 100.0%; Pred. No. 6.2e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YQTKVNLSSAISKPCQRETPEG 22
Db 78 YQTKVNLSSAISKPCQRETPEG 99

RESULT 4

US-07-668-517-2
Sequence 2, Application US/07668517
Patent No. 5262309

GENERAL INFORMATION:

APPLICANT: SATOSHI NAKAMURA et al.
TITLE OF INVENTION: No. 5262309el Physiologically Active
TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism
TITLE OF INVENTION: Cell, Pharmaceutical Composition and Method of Recovering
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb
COMPUTER: IBM Compatible

US-07-668-517-3

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Query Match          100.0%; Score 115; DB 1; Length 149;
Best Local Similarity 100.0%; Pred. No. 6.3e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YOTKVNLLSAIKSPCQRETPEG 22
   |||||
Db 79 YOTKVNLLSAIKSPCQRETPEG 100

RESULT 7
US-07-668-517-16
; Sequence 16, Application US/07668517
; Patent No. 5262309
; GENERAL INFORMATION:
; APPLICANT: Satoshi NAKAMURA et al.
; TITLE OF INVENTION: No. 5262309el Physiologically Active
; TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism
; TITLE OF INVENTION: Cell, Pharmaceutical Composition and Method of Recovering
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/668,517
; FILING DATE: 19910322
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Matthew Jacob
; REGISTRATION NUMBER: 25,154
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX: 202-371-8856
; TELEX:
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 149 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; US-07-668-517-16

Query Match          100.0%; Score 115; DB 1; Length 149;
Best Local Similarity 100.0%; Pred. No. 6.3e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YOTKVNLLSAIKSPCQRETPEG 22
   |||||
Db 79 YOTKVNLLSAIKSPCQRETPEG 100

RESULT 8
US-07-668-517-4
; Sequence 4, Application US/07668517
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; Patent No. 5262309
; GENERAL INFORMATION:
; APPLICANT: Satoshi NAKAMURA et al.
; TITLE OF INVENTION: No. 5262309el Physiologically Active
; TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism
; TITLE OF INVENTION: Cell, Pharmaceutical Composition and Method of Recovering
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/668,517
; FILING DATE: 19910322
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Matthew Jacob
; REGISTRATION NUMBER: 25,154
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX: 202-371-8856
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 150 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; US-07-668-517-4

Query Match          100.0%; Score 115; DB 1; Length 150;
Best Local Similarity 100.0%; Pred. No. 6.4e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YOTKVNLLSAIKSPCQRETPEG 22
   |||||
Db 80 YOTKVNLLSAIKSPCQRETPEG 101

RESULT 9
US-07-668-517-5
; Sequence 5, Application US/07668517
; Patent No. 5262309
; GENERAL INFORMATION:
; APPLICANT: Satoshi NAKAMURA et al.
; TITLE OF INVENTION: No. 5262309el Physiologically Active
; TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism
; TITLE OF INVENTION: Cell, Pharmaceutical Composition and Method of Recovering
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
```

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/668,517
FILING DATE: 19910322
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Matthew Jacob
REGISTRATION NUMBER: 25,154
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 150 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-07-668-517-5

Query Match 100.0%; Score 115; DB 1; Length 150;
Best Local Similarity 100.0%; Pred. No. 6.4e-12; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YQTKVNLLSAIKSPCQRETPG 22
|||||
Db 80 YQTKVNLLSAIKSPCQRETPG 101

RESULT 10
US-07-668-517-6
Sequence 6, Application us/07668517
Patent No. 5262309
GENERAL INFORMATION:
APPLICANT: Satoshi NAKAMURA et al.
TITLE OF INVENTION: No. 5262309el Physiologically Active
TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism
TITLE OF INVENTION: Cell, Pharmaceutical Composition and Method of Recovering
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/668,517
FILING DATE: 19910322
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Matthew Jacob

REGISTRATION NUMBER: 25,154
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 150 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-07-668-517-6

Query Match 100.0%; Score 115; DB 1; Length 150;
Best Local Similarity 100.0%; Pred. No. 6.4e-12; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YQTKVNLLSAIKSPCQRETPG 22
|||||
Db 80 YQTKVNLLSAIKSPCQRETPG 101

RESULT 11
US-07-668-517-8
Sequence 8, Application US/07668517
Patent No. 5262309
GENERAL INFORMATION:
APPLICANT: Satoshi NAKAMURA et al.
TITLE OF INVENTION: No. 5262309el Physiologically Active
TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism
TITLE OF INVENTION: Cell, Pharmaceutical Composition and Method of Recovering
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/668,517
FILING DATE: 19910322
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Matthew Jacob
REGISTRATION NUMBER: 25,154
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 150 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY:

;
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
US-07-668-517-8

Query Match 100.0%; Score 115; DB 1; Length 150;
Best Local Similarity 100.0%; Pred. No. 6.4e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YQTKVNLLSAIKSPCQRETPEG 22
|||||
Db 80 YQTKVNLLSAIKSPCQRETPEG 101

RESULT 12

US-07-668-517-9
; Sequence 9, Application US/07668517
; Patent No. 5262309

; GENERAL INFORMATION:

; APPLICANT: Satoshi NAKAMURA et al.

; TITLE OF INVENTION: No. 5262309el Physiologically Active

; TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism

; TITLE OF INVENTION: Cell, Pharmaceutical Composition and Method of Recovering

; NUMBER OF SEQUENCES: 50

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Wenderoth, Lind & Ponack

; STREET: 805 Fifteenth Street, N.W., #700

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: DisplayWrite

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/668,517

; FILING DATE: 19910322

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Matthew Jacob

; REGISTRATION NUMBER: 25,154

; REFERENCE/DOCKET NUMBER:

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-371-8850

; TELEFAX: 202-371-8856

; TELEX:

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 150 amino acids

; TYPE: AMINO ACID

; STRANDEDNESS: single

; TOPOLOGY: linear

; FEATURE:

; NAME/KEY:

; LOCATION:

; IDENTIFICATION METHOD:

; OTHER INFORMATION:

US-07-668-517-9

Query Match 100.0%; Score 115; DB 1; Length 150;

Best Local Similarity 100.0%; Pred. No. 6.4e-12;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YQTKVNLLSAIKSPCQRETPEG 22
|||||
Db 80 YQTKVNLLSAIKSPCQRETPEG 101

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; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/668,517
; FILING DATE: 19910322
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Matthew Jacob
; REGISTRATION NUMBER: 25,154
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX: 202-371-8856
; TELEX:
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 150 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; US-07-668-517-11

Query Match 100.0%; Score 115; DB 1; Length 150;
Best Local Similarity 100.0%; Pred. No. 6.4e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YQTKVNLLSAIKSPCQRETPG 22
Db 80 YQTKVNLLSAIKSPCQRETPG 101

RESULT 15
US-07-668-517-12
; Sequence 12, Application US/07668517
; Patent No. 5262309
; GENERAL INFORMATION:
; APPLICANT: Satoshi NAKAMURA et al.
; TITLE OF INVENTION: No. 5262309el Physiologically Active
; TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism
; TITLE OF INVENTION: Cell, Pharmaceutical Composition and Method of Recovering
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/668,517
; FILING DATE: 19910322
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
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; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Matthew Jacob
; REGISTRATION NUMBER: 25,154
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX: 202-371-8856
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 150 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; US-07-668-517-12

Query Match 100.0%; Score 115; DB 1; Length 150;
Best Local Similarity 100.0%; Pred. No. 6.4e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YQTKVNLLSAIKSPCQRETPG 22
Db 80 YQTKVNLLSAIKSPCQRETPG 101

Search completed: December 4, 2002, 13:24:29
Job time : 14.3158 secs
```


GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 4, 2002, 13:30:18 ; Search time 14 seconds
(without alignments)
109.868 Million cell updates/sec

Title: US-09-754-004-1

Perfect score: 89

Sequence: 1 YSOVLFKQGCGPSTHV 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 2770

Minimum DB seq length: 0

Maximum DB seq length: 16

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR-73.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	32.6	12	2 A61309	glycoprotein hormo
2	26	29.2	15	2 A48630	bothrojaracin - ja
3	24	27.0	15	2 I49407	placental calcium-
4	22	24.7	9	2 S15850	vitamin D3 26-mono
5	22	24.7	9	2 A60522	sperm-activating p
6	22	24.7	10	2 I48778	small nuclear ribo
7	22	24.7	13	2 PH1309	Ig heavy chain DJ
8	22	24.7	14	2 I39753	nitrogenase (EC 1.
9	22	24.7	14	2 S23376	collagen alpha cha
10	22	24.7	15	2 S05700	insulin-like growt
11	21	23.6	9	2 A91466	oxytocin - spotted
12	21	23.6	9	2 A92774	oxytocin - finback
13	21	23.6	9	2 A93147	oxytocin - Austral
14	21	23.6	9	2 A93408	oxytocin - rabbit
15	21	23.6	9	2 B90667	oxytocin - beta ch
16	21	23.6	9	2 D24180	fibrinogen beta ch
17	21	23.6	9	2 S06375	arginine vasotocin
18	21	23.6	9	2 B61364	vasotocin - common
19	21	23.6	10	2 A61131	hydrin 2 - bullfro
20	21	23.6	12	2 A33900	hydrin 1 - African
21	21	23.6	14	2 PH1322	Ig heavy chain DJ
22	21	23.6	15	2 PA0034	protein QA300024 -
23	21	23.6	15	2 PT0085	protein QA600027 -
24	21	23.6	15	2 C24687	T-cell receptor be
25	21	23.6	16	2 A28587	T-cell receptor al
26	20.5	23.0	13	2 A54326	glandular kallikre
27	20.5	23.0	16	2 H41299	T-cell receptor al
28	20	22.5	8	2 S63493	dissimilatory sulf
29	20	22.5	11	2 S23373	T-cell receptor al

30	20	22.5	13	2 A60379	factor X activator
31	20	22.5	14	2 A39239	actin 8 - slime mo
32	20	22.5	15	2 PA0054	protein QF200017 -
33	20	22.5	15	2 A32921	beaded-chain filam
34	20	22.5	16	2 G24687	T-cell receptor be
35	19	21.3	7	2 I50210	gene c-rel protein
36	19	21.3	7	2 PT0671	T-cell receptor be
37	19	21.3	9	2 D28854	fibrinopeptide B -
38	19	21.3	11	2 A33917	dihydroorotase (EC
39	19	21.3	11	2 P00029	33K protein 3218 -
40	19	21.3	12	2 S26556	T-cell receptor be
41	19	21.3	12	2 S26552	T-cell receptor be
42	19	21.3	12	2 C33099	148K exoantigen -
43	19	21.3	15	2 S61438	hypothetical prote
44	19	21.3	15	2 PA0055	protein QF200007 -
45	19	21.3	15	2 A08416	lombricine kinase

ALIGNMENTS

RESULT 1

A61309

glycoprotein hormones alpha chain - hamster (fragment)

N:Alternate names: chorionadotropin alpha chain; luteinizing hormone alpha chain; 1

C:Species: Cricetinae gen. sp. (hamster)

C>Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 07-May-1999

C:Accession: A61309

R:Glenn, S.D.; Nahm, H.S.; Greenwald, G.S.; Ward, D.N.

Endocrinology 111, 1263-1269, 1982

A:Title: Isolation and characterization of hamster luteinizing hormone.

A:Reference number: A61309; MUID:83003498; PMID:6889489

A:Accession: A61309

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-12 <GLS>

C:Superfamily: glycoprotein hormones alpha chain

C:Keywords: glycoprotein

Query Match 32.6%; Score 29; DB 2; Length 12;

Best Local Similarity 71.4%; Pred. No. 1.8e+02;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 FKQGCGP 12

Db 6 FTMQGCP 12

RESULT 2

A48630

bothrojaracin - jararaca (fragment)

N:Alternate names: thrombin inhibitor

C:Species: Bothrops jararaca (Jararaca)

C>Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995

C:Accession: A48630

R:Zingali, R.B.; Jandrot-Perrus, M.; Guillin, M.C.; Bon, C.

Biochemistry 32, 10794-10802, 1993

A:Title: Bothrojaracin, a new thrombin inhibitor isolated from Bothrops jararaca veno

A:Reference number: A48630; MUID:94002075; PMID:8399228

A:Accession: A48630

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-16 <ZIN>

A:Experimental source: venom

A>Note: sequence extracted from NCBI backbone (NCBIP:138787)

Query Match 29.2%; Score 26; DB 2; Length 16;

Best Local Similarity 100.0%; Pred. No. 7.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 GQGC 11

Db 10 GQGC 13

RESULT 3

I49407
placental calcium-binding protein - western wild mouse (fragment)
C:Species: Mus spretus (western wild mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 29-Sep-1999
C:Accession: I49407
R:Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, J.H.
Mamm. Genome 5, 349-355, 1994
A:Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.
A:Reference number: I48934; MUID:94319082; PMID:8043949
A:Accession: I49407
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-15 <RES>
A:Cross-references: EMBL:U05696; NID:g497016; PID:AAA61936.1; PID:g497017
C:Superfamily: S-100 protein; calmodulin repeat homology
C:Keywords: calcium binding; EF hand

Query Match 27.0%; Score 24; DB 2; Length 15;
Best Local Similarity 75.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 QGCP 12
Db 5 EGCP 8

RESULT 4

S15850
vitamin D3 26-monooxygenase (EC 1.14.14.-) cytochrome P450 27 - pig (fragment)
N:Alternate names: cytochrome P450(26); vitamin D3 26-hydroxylase
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 23-Apr-1993 #sequence_revision 23-Apr-1993 #text_change 05-Mar-1999
C:Accession: S15850
R:Bergman, T.; Postlind, H.
Biochem. J. 276, 427-432, 1991
A:Title: Characterization of mitochondrial cytochromes P-450 from pig kidney and liver
A:Reference number: S15850; MUID:91264797; PMID:2049072
A:Accession: S15850
A:Molecule type: protein
A:Residues: 1-9 <BIO>
C:Genetics:
A:Gene: CYP27
C:Superfamily: unassigned cytochrome P450; cytochrome P450 homology
C:Keywords: heme; mitochondrion; monooxygenase; oxidoreductase; transmembrane protein

Query Match 24.7%; Score 22; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KGQG 10
Db 3 KGQG 6

RESULT 5

A60522
sperm-activating peptide SAP-IV - sea urchin (Diadema setosum)
C:Species: Diadema setosum
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
C:Accession: A60522
R:Yoshino, K.I.; Kurita, M.; Yamaguchi, M.; Nomura, K.; Takao, T.; Shimonishi, Y.; Suzuki, K.
Comp. Biochem. Physiol. B 95, 423-429, 1990
A:Title: A species-specific sperm-activating peptide from the egg jelly of the sea urchin
A:Reference number: A60522; MUID:90227916; PMID:2158412
A:Accession: A60522
A:Molecule type: protein
A:Residues: 1-9 <VOS>
C:Superfamily: unassigned animal peptides
F:2-9/disulfide bonds: #status experimental

Query Match 24.7%; Score 22; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GCP 12
Db 1 GCP 3

RESULT 6

I48778
small nuclear ribonucleoprotein E - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: I48778
R:Fautsch, M.P.; Thompson, M.A.; Holicky, E.L.; Schultz, P.J.; Hallett, J.B.; Wieben, G.
Genomics 14, 883-890, 1992
A:Title: Conservation of coding and transcriptional control sequences within the snRN
A:Reference number: A44368; MUID:93122798; PMID:1478669
A:Accession: I48778
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-10 <RES>
A:Cross-references: EMBL:X65703; NID:g312006; PIDN:CAA46625.1; PID:g312007

Query Match 24.7%; Score 22; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 FKQG 10
Db 3 YRQG 7

RESULT 7

PHI309
Ig heavy chain DJ region (clone C770-101) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PHI309
R:Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A:Title: Predominance of fetal type DJH joining in young children with B precursor ly
A:Reference number: PHI302; MUID:93094761; PMID:1460419
A:Accession: PHI309
A:Molecule type: DNA
A:Residues: 1-13 <WAS>
C:Keywords: heterotrimer; immunoglobulin

Query Match 24.7%; Score 22; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 CPST 14
Db 5 CPPT 8

RESULT 8

I39753
nitrogenase (EC 1.18.6.1) - Azospirillum brasilense (fragment)
N:Alternate names: dinitrogenase reductase
C:Species: Azospirillum brasilense
C>Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 19-Jan-2001
C:Accession: I39753
R:Zhang, Y.; Burris, R.H.; Roberts, G.P.
J. Bacteriol. 174, 3364-3369, 1992
A:Title: Cloning, sequencing, mutagenesis, and functional characterization of draft an
A:Reference number: I39751; MUID:92250433; PMID:1577701
A:Accession: I39753
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-14 <RES>

A;Cross-references: GB:M87319; NID:gi42411; PIDN:AAA22182.1; PID:gi42414
C;Keywords: ATP; nitrogen fixation; oxidoreductase

Query Match 24.7%; Score 22; DB 2; Length 14;
Best Local Similarity 37.5%; Pred. No. 3.1e+03;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 VLFKQGQC 11
: : :
Db 5 IFFEKPGC 12

RESULT 9

S23376 collagen alpha chain - polychaete (Alvinella pompejana) (fragment)

C;Species: Alvinella pompejana
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 29-May-1998
C;Accession: S23376
R;Gaili, F.; Wiedemann, H.; Mann, K.; Kuehn, K.; Timpl, R.; Engel, J.
J. Mol. Biol. 221, 209-223, 1991
A;Title: Molecular characterization of cuticle and interstitial collagens from worms col
A;Reference number: S17581; MUID:92015209; PMID:1920405
A;Accession: S23376
A;Molecule type: protein
A;Residues: 1-14 <GAI>

Query Match 24.7%; Score 22; DB 2; Length 14;
Best Local Similarity 57.1%; Pred. No. 3.1e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 FKQGQPC 12
: : :
Db 1 FOAQGGP 7

RESULT 10

S05700

insulin-like growth factor-binding protein, adult - human (fragment)

C;Species: Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 18-Jun-1993
C;Accession: S05700
R;Roghani, M.; Hossenlopp, P.; Lepage, P.; Balland, A.; Binoux, M.
FEBS Lett. 255, 253-258, 1989
A;Title: Isolation from human cerebrospinal fluid of a new insulin-like growth factor-b
A;Reference number: S05699; MUID:90005986; PMID:2551732
A;Accession: S05700
A;Molecule type: protein
A;Residues: 1-15 <ROG>

Query Match 24.7%; Score 22; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KGQG 10
: : :
Db 5 KGQG 8

RESULT 11

A91466

oxytocin - hippopotamus

N;Alternate names: neurophysin I
C;Species: Hippopotamus amphibius (hippopotamus)
C;Date: 30-Oct-1992 #sequence_revision 30-Oct-1992 #text_change 20-Mar-1998
C;Accession: A91466; MUID:401450; B01450
R;Ferguson, D.R.; Pickering, B.T.
Gen. Comp. Endocrinol. 13, 425-429, 1969
A;Title: Arginine and lysine vasopressins in the hippopotamus neurohypophysis.
A;Reference number: A91466; MUID:7123719; PMID:5406007
A;Accession: A91466
A;Molecule type: protein
A;Residues: 1-9 <FER>

C;Comment: Oxytocin is followed by neurophysin 1 in the precursor.
C;Superfamily: oxytocin-neurophysin
C;Keywords: amidated carboxyl end; hormone; hypothalamus
F;1-6/bisulfide bonds: #status predicted
F;9/Modified site: amidated carboxyl end (Gly) #status predicted

Query Match 23.6%; Score 21; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 QGCP 12
: : :
Db 4 QNCP 7

RESULT 12

A92774

oxytocin - spotted ratfish

N;Alternate names: neurophysin I
C;Species: Hydrotaea colliei (spotted ratfish)
C;Date: 30-Oct-1992 #sequence_revision 30-Oct-1992 #text_change 20-Mar-1998
C;Accession: A92774; A01450; B01450
R;Pickering, B.T.; Heller, H.
J. Endocrinol. 45, 597-606, 1969
A;Title: Oxytocin as a neurohypophysial hormone in the holocephalian elasmobranch fis
A;Reference number: A92774; MUID:70088110; PMID:5366118
A;Accession: A92774
A;Molecule type: protein
A;Residues: 1-9 <PIC>

C;Comment: Oxytocin is followed by neurophysin 1 in the precursor.
C;Superfamily: oxytocin-neurophysin
C;Keywords: amidated carboxyl end; hormone; hypothalamus
F;1-6/bisulfide bonds: #status predicted
F;9/Modified site: amidated carboxyl end (Gly) #status predicted

Query Match 23.6%; Score 21; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 QGCP 12
: : :
Db 4 QNCP 7

RESULT 13

A93147

oxytocin - finback whale

N;Alternate names: neurophysin I
C;Species: Balaenoptera physalus (finback whale, common rorqual)
C;Date: 30-Oct-1992 #sequence_revision 30-Oct-1992 #text_change 20-Mar-1998
C;Accession: A93147; A01450; B01450
R;Acher, R.; Chauvet, J.; Chauvet, M.T.
Nature 201, 191-192, 1964
A;Title: Isolation of finback whale oxytocin and vasopressin.
A;Reference number: A93147
A;Accession: A93147
A;Molecule type: protein
A;Residues: 1-9 <ACH>

C;Comment: Oxytocin is followed by neurophysin 1 in the precursor.
C;Superfamily: oxytocin-neurophysin
C;Keywords: amidated carboxyl end; hormone; hypothalamus
F;1-6/bisulfide bonds: #status experimental
F;9/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 23.6%; Score 21; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 QGCP 12
: : :
Db 4 QNCP 7

RESULT 14

A93408
oxytocin - Australian echidna
N:Alternate names: neurophysin I
N:Contains: neurophysin 1; oxytocin
C:Species: tachyglossus aculeatus (Australian echidna)
C>Date: 30-Oct-1992 #sequence_revision 30-Oct-1992 #text_change 20-Mar-1998
C:Accession: A93408; A01450; B01450
R:Acher, R.; Chauvet, J.; Chauvet, M.T.
Nature New Biol. 244, 124-126, 1973
A:Title: Neurohypophysial hormones and evolution of tetrapods.
A:Reference number: A93408; MUID:73223515; PMID:4515919

A:Accession: A93408
A:Molecule type: protein
A:Residues: 1-9 <ACH>
C:Comment: Oxytocin is followed by neurophysin 1 in the precursor.
C:Superfamily: oxytocin-neurophysin
C:Keywords: amidated carboxyl end; hormone; hypothalamus
F:1-6/Disulfide bonds: #status predicted
F:9/Modified site: amidated carboxyl end (Gly) #status predicted

Query Match 23.6%; Score 21; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 9 QGCP 12
| | |
Db 4 QNCP 7

RESULT 15

B90667
oxytocin - rabbit
N:Alternate names: neurophysin I
N:Contains: neurophysin 1; oxytocin
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 30-Oct-1992 #sequence_revision 30-Oct-1992 #text_change 20-Mar-1998
C:Accession: B90667; A01450; B01450
R:Chauvet, J.; Chauvet, M.T.; Acher, R.
Biochimie 53, 1099-1104, 1971
A:Title: Evolution des hormones neurohypophysaires: isolement des principes actifs du la
A:Reference number: A90667; MUID:72215060; PMID:5150741

A:Accession: B90667
A:Molecule type: protein
A:Residues: 1-9 <CHA>
C:Comment: Oxytocin is followed by neurophysin 1 in the precursor.
C:Superfamily: oxytocin-neurophysin
C:Keywords: amidated carboxyl end; hormone; hypothalamus
F:1-6/Disulfide bonds: #status experimental
F:9/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 23.6%; Score 21; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 9 QGCP 12
| | |
Db 4 QNCP 7

Search completed: December 4, 2002, 13:32:29
Job time : 14 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 4, 2002, 13:25:08 ; Search time 10 seconds
(without alignments)
66.362 Million cell updates/sec

Title: US-09-754-004-1

Perfect score: 89

Sequence: 1 YSQVLFKGGGCPSTHV 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 822

Minimum DB seq length: 0

Maximum DB seq length: 16

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	21	23.6	9	1 FIBB_ERYPA	P19346 erythrocebu
2	21	23.6	9	1 OXYT_BUFRE	P42995 bufo regula
3	21	23.6	9	1 OXYT_CYPCA	P32879 cyprinus ca
4	21	23.6	9	1 OXYT_RABIT	P32878 eryctologia
5	21	23.6	9	1 OXYV_SQUAC	P43000 squalus aca
6	20	22.5	15	1 PH2_PERAM	P82695 periplaneta
7	19	21.3	9	1 FIBB_PAPAN	P19344 papio anubi
8	19	21.3	15	1 KLOM_LUMTE	P11918 lumbricus t
9	18	20.2	8	1 VGLG_HSV2B	P42998 herpes simp
10	18	20.2	9	1 OXYT_EISFO	P42998 eisenia foe
11	18	20.2	9	1 PCLR_DIAAB	P81179 diaprepes a
12	18	20.2	10	1 BPP_VIPAS	P31351 vipera aspi
13	18	20.2	12	1 H2AX_ONCMY	P83327 oncorhynch
14	18	20.2	16	1 CXA2_CONNA	P56636 conus magus
15	17	19.1	9	1 CONO_CONGE	P05486 conus geogr
16	17	19.1	9	1 CONO_CONST	P05487 conus stria
17	17	19.1	9	1 FIBB_MACFU	P19345 macaca fusc
18	17	19.1	9	1 OXYT_OCTVU	P80027 octopus vul
19	17	19.1	11	1 BPPB_AKGHA	P01021 agkistrodon
20	17	19.1	14	1 UN37_CLOPA	P81358 clostridium
21	17	19.1	15	1 ACT_FINFS	P81085 pinus pinas
22	17	19.1	15	1 CX3A_CONQU	P58841 conus querc
23	17	19.1	15	1 CX3B_CONQU	P58842 conus querc
24	17	19.1	16	1 KTRC_ARENA	P11917 arenicola m
25	17	19.1	16	1 LPK1_LOCMI	P20404 locusta mig
26	17	19.1	16	1 MMPX_SOLTU	P80501 solanum tub
27	16	18.0	8	1 AC1_THUAL	P18691 thunnus alb
28	16	18.0	8	1 GLUR_HUMAN	P02729 homo sapien
29	16	18.0	9	1 COW_CONVE	P83047 conus ventr
30	16	18.0	9	1 DNFI_LOCMI	P16339 locusta mig
31	16	18.0	9	1 FIBB_PAPHA	P19343 papio hamad
32	16	18.0	9	1 ISOT_CYPCA	P42993 cyprinus ca
33	16	18.0	9	1 OXYA_SCYCA	P42996 scyllorhinu

34 16 18.0 9 1 OXYA_SQUAC P42999 squalus aca
35 16 18.0 9 1 OXYT_SCYCA P42997 scyllorhinu
36 16 18.0 9 1 OXYT_RAJCL P42994 raja clavav
37 16 18.0 9 1 SNA_STOVA P24047 stomopneute
38 16 18.0 9 1 THIF_PIG P01255 sus scrofa
39 16 18.0 10 1 AH3_PRUSE P29261 prunus sero
40 16 18.0 10 1 AKHX_LOCMI P81626 locusta mig
41 16 18.0 11 1 CX5A_CONAL P58848 conus aulic
42 16 18.0 11 1 CX5B_CONAL P58849 conus aulic
43 16 18.0 12 1 CXAL_CONIM P50983 conus imper
44 16 18.0 13 1 AH4_PRUSE P29262 prunus sero
45 16 18.0 13 1 CRTC_BOVIN P28489 bos taurus

ALIGNMENTS

RESULT 1
FIBB_ERYPA STANDARD; PRT; 9 AA.
AC P19346;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Erythrocebus patas (Red guenon) (Hussar).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Erythrocebus.
OX NCBI_TaxID=9538;
RN [1]
RP SEQUENCE.
RA MEDLINE=85289140; PubMed=3928610;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and
RT patas monkey (Erythrocebus patas): their amino acid sequences,
RT restricted mutations, and a molecular phylogeny for macaques,
RT guenons, and baboons.";
RL J. Biochem. 97:1487-1492(1985).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
PIR: D24180; D24180.
DR InterPro: IPR002181; Fibrinogen_C.
DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1020 MW; 69FE7879C732CB1B CRC64;

Query Match 23.6%; Score 21; DB 1; Length 9;
Best Local Similarity 57.1%; Pred. NO. 1.1e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 3 QVLFKGG 9
Db 3 EVLFGR 9

RESULT 2
OXYT_BUFRE STANDARD; PRT; 9 AA.
AC P42995;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

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DE Seritocin.
OS Bufo regularis (Leopard toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Bufonidae;
OC Bufo.
OX NCBI_TaxID=8390;
RN [1]
RP SEQUENCE.
RC TISSUE=Pituitary neurointermediate lobe;
RX MEDLINE=96059313; PubMed=7591488;
RA Chauvet J., Michel G., Ouedraogo Y., Chou J., Chalt B.T., Acher R.;
RT "A new neurohypophyseal peptide, seritocin ([Ser5,Ile8]-oxytocin),
RT identified in a dryness-resistant African toad, Bufo regularis.";
RL Int. J. Pept. Protein Res. 45:482-487(1995).
CC -!- FUNCTION: DEVOID OF OXYTOCIN ACTIVITY.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro; IPR000981; Neurohyp_horm.
DR InterPro; IPR001230; Prenyl_site.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; FALSE_NEG.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
FT SEQUENCE 9 AA; 983 MW; 17FF476E5A5A6D04B CRC64;
SQ
Query Match 23.6%; Score 21; DB 1; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.1e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 9 QGCP 12
DB 4 QSCP 7
RESULT 3
OXYT_CYPCA STANDARD; PRT; 9 AA.
AC P23879;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Vasotocin.
OS Cyprinus carpio (Common carp), and
OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962, 7757;
RN [1]
RP SEQUENCE.
RC SPECIES=C. carpio; TISSUE=Pituitary;
RA Acher R., Chauvet J., Chauvet M.-T., Crepy D.;
RT "Characterization of neurohypophyseal hormones from a fresh water bony
RT fish, the carp (Cyprinus carpio). Comparison with hormones from sea
RT water bony fishes.";
RL Comp. Biochem. Physiol. 14:245-254(1965).
RN [2]
RP SEQUENCE.
RC SPECIES=P. marinus; TISSUE=Pituitary;
RX MEDLINE=88225976; PubMed=3371648;
RA Lane T.F., Sower S.A., Kawachi H.;
RT "Arginine vasotocin from the pituitary gland of the lamprey
RT (Petromyzon marinus): isolation and amino acid sequence.";
RL Gen. Comp. Endocrinol. 70:152-157(1988).
CC -!- FUNCTION: ANTIDIURETIC HORMONE.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR PIR; B61364; B61364.
DR InterPro; IPR000981; Neurohyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID- 1 6
FT MOD_RES 9 9
FT SEQUENCE 9 AA; 983 MW; 17FF476E5A5A6D04B CRC64;
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FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 1053 MW; 17EB176EB456D04B CRC64;
Query Match 23.6%; Score 21; DB 1; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.1e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 9 QGCP 12
DB 4 QSCP 7
RESULT 4
OXYT_RABIT STANDARD; PRT; 9 AA.
AC P23878; P01188;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Oxytocin (Oxytocin).
OS Oryctolagus cuniculus (Rabbit),
OS Hippopotamus amphibius (Hippopotamus),
OS Balanoptera physalus (Finback whale), (Common rorqual), and
OS Tachyglus aculeatus aculeatus (Spotted ratfish) (Pacific ratfish).
OS Hydroglus collei (Spotted ratfish) (Pacific ratfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986, 9833, 9770, 49271, 7873;
RN [1]
RP SEQUENCE.
RC SPECIES=Rabbit;
RX MEDLINE=72215060; PubMed=5150741;
RA Chauvet J., Chauvet M.-T., Acher R.;
RT "Evolution of neurohypophyseal hormones: isolation of active
RT principles from rabbits and rats.";
RL Biochimie 53:1099-1104(1971).
RN [2]
RP SEQUENCE.
RC SPECIES=H. amphibius;
RX MEDLINE=71232719; PubMed=5406007;
RA Ferguson D.R., Pickering B.T.;
RT "Arginine and lysine vasopressins in the hippopotamus
RT neurohypophysis.";
RL Gen. Comp. Endocrinol. 13:425-429(1969).
RN [3]
RP SEQUENCE.
RC SPECIES=B. physalus;
RA Acher R., Chauvet J., Chauvet M.-T.;
RT "Isolation of finback whale oxytocin and vasopressin.";
RL Nature 201:191-192(1964).
RN [4]
RP SEQUENCE.
RC SPECIES=A. aculeatus;
RX MEDLINE=73223515; PubMed=4515919;
RA Acher R., Chauvet J., Chauvet M.-T.;
RT "Neurohypophyseal hormones and evolution of tetrapods.";
RL Nature New Biol. 244:124-126(1973).
RN [5]
RP SEQUENCE.
RC SPECIES=H. collei;
RX MEDLINE=70088110; PubMed=5366118;
RA Pickering B.T., Heller H.;
RT "Oxytocin as a neurohypophyseal hormone in the holoccephalian
RT elasmobranch fish, Hydroglus collei.";
RL J. Endocrinol. 45:597-606(1969).
CC -!- FUNCTION: OXYTOCIN CAUSES CONTRACTION OF THE SMOOTH MUSCLE OF THE
CC UTERUS AND OF THE MAMMARY GLAND.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR PIR; A91466; A91466.
DR PIR; A92774; A92774.
DR PIR; A93147; A93147.
DR PIR; A93408; A93408.
DR PIR; B90667; B90667.
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DR PDB; 1XY1; 15-OCT-90.
DR PDB; 1XY2; 15-OCT-90.
DR InterPro: IPR000981; Neurohyp.horm.
DR InterPro: IPR001230; Prenyl_site.
DR Pfam: PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Hypothalamus; Amidation; 3D-structure.
FT DISULFID 1 6
FT MOD_RES 9 9
FT SEQUENCE 9 AA; 1010 MW; 17FB3765EB456D04B CRC64;
SQ SEQUENCE 9 AA; 1010 MW; 17FB3765EB456D04B CRC64;

Query Match 23.6%; Score 21; DB 1; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.1e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 QGCP 12
DB 4 QNCP 7

RESULT 5
OXYV_SQUAC STANDARD; PRT; 9 AA.
AC P43000;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Valitocin.
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Squaloidae; Squalidae; Squalus.
OX NCBI_TaxID=7797;
RN [1]
RP SEQUENCE.
RX MEDLINE=73031727; PubMed=5083097;
RA Acher R., Chauvet J., Chauvet M.-T.;
RT "Phylogeny of the neurohypophysial hormones. Two new active peptides isolated from a cartilaginous fish, Squalus acanthias.";
RL Eur. J. Biochem. 29:12-19(1972).
RN [2]
RP SEQUENCE.
RX MEDLINE=72128038; PubMed=4622083;
RA Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;
RT "Identification of 2 new neurohypophysial hormones, valitocin (Val8-oxytocin) and aspartocin (Asn4-oxytocin) in a selachian fish, the spiny dog-fish (Squalus acanthias).";
RL C. R. Acad. Sci., D, Sci. Nat. 274:313-316(1972).
CC -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro: IPR000981; Neurohyp.horm.
DR Pfam: PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
FT SEQUENCE 9 AA; 996 MW; 17EDD76EB456D04B CRC64;
SQ SEQUENCE 9 AA; 996 MW; 17EDD76EB456D04B CRC64;

Query Match 23.6%; Score 21; DB 1; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.1e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 QGCP 12
DB 4 QNCP 7

RESULT 6
PH2_PERAM STANDARD; PRT; 15 AA.
AC P82695;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

Peptide hormone 2 (Pea-VEAacid 2).
Periplaneta americana (American cockroach).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
Blattoidea; Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE.
RC TISSUE=Abdominal perisymphathetic organs;
RA Predel R.;
RL Submitted (JUL-2000) to the SWISS-PROT data bank.
CC -1- FUNCTION: UNKNOWN.
KW Neuropeptide.
SQ SEQUENCE 15 AA; 1603 MW; F353DC8B1F92B8BD CRC64;

Query Match 22.5%; Score 20; DB 1; Length 15;
Best Local Similarity 60.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 PSTHV 16
DB 5 PGSHV 9

RESULT 7
FIBB_PAPAN STANDARD; PRT; 9 AA.
AC P19344;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Papio.
OX NCBI_TaxID=9555;
RN [1]
RP SEQUENCE.
RX MEDLINE=84161822; PubMed=6423621;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas, and Theropithecus gelada): their amino acid sequences and evolutionary rates and a molecular phylogeny for the baboons.";
RL J. Biochem. 94:1973-1978(1983).
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET AGGREGATION.
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR PIR; D28854; D28854.
DR InterPro: IPR002181; Fibrinogen_C.
DR PROSITE; PS00514; FIBRINAG_C_DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9
FT NON_TER 9 9
FT SEQUENCE 9 AA; 1076 MW; DDFE6409C7287B06 CRC64;
SQ SEQUENCE 9 AA; 1076 MW; DDFE6409C7287B06 CRC64;

Query Match 21.3%; Score 19; DB 1; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.1e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 LFKGQ 9
DB 5 LFRGR 9

RESULT 8
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KLOM_LUMTE
ID KLOM_LUMTE STANDARD; PRT; 15 AA..
AC P11918;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Lombricine kinase (EC 2.7.3.5) (LK) (Fragment).
OS Lumbricus terrestris (Common earthworm).
OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
OC Lumbricina; Lumbricidae; Lumbricus.
OX NCBI_TaxID=6398;
RN [1]
RP SEQUENCE.
RX MEDLINE=72066544; PubMed=5128744;
RA "Comparative structural studies of the active site of ATP: guanidine phosphotransferases. The essential cysteine tryptic peptide of lombricine kinase from Lumbricus terrestris muscle.";
RL Eur. J. Biochem. 22:585-592(1971).
CC -!- CATALYTIC ACTIVITY: ATP + lombricine = ADP + N-phospholombricine.
CC -!- SUBUNIT: HOMODIMER.
CC -!- SIMILARITY: BELONGS TO THE ATP:GUANIDO PHOSPHOTRANSFERASE FAMILY.
DR InterPro: A08416; A08416.
DR InterPro: IPR000749; ATP-gua_Ptrans.
DR PROSITE: PS00112; GUANIDO_KINASE; 1.
KW Kinase; Transferase.
FT NON_TER 1 1
FT ACT_SITE 6 6
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1565 MW; 2A45FEF6140E90C4 CRC64;

Query Match 21.3%; Score 19; DB 1; Length 15;
Best Local Similarity 33.3%; Pred. No. 3.3e+03;
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 11 CPSTHV 16
|| :||
Db 6 CPGSNL 11

RESULT 9
VGLG_HSV2B VGLG_HSV2B STANDARD; PRT; 8 AA..
AC P81780;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Glycoprotein G (Fragment).
OS Herpes simplex virus (type 2 / strain B4327UR).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=103921;
RN [1]
RP SEQUENCE.
RA Liljeqvist J.-A., Svennerholm B., Bergstrom T.;
RL Submitted (APR-1999) to the SWISS-PROT data bank.
CC -!- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1 AND
CC 2: GH, GB, GC, GG, GD, GI, AND GE.
CC -!- MISCELLANEOUS: GLYCOPROTEIN G IS MUCH LARGER IN HSV-2 THAN IN
CC HSV-1.
KW Glycoprotein.
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 583 MW; 7847686772C865B8 CRC64;

Query Match 20.2%; Score 18; DB 1; Length 8;
Best Local Similarity 60.0%; Pred. No. 1.1e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 GCGCP 12
|| :||
Db 1 GSGVP 5

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RESULT 10
OXYT_EISFO OXYT_EISFO STANDARD; PRT; 9 AA..
AC P42998;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Annetocin.
OS Eisenia foetida (Common brandling worm) (Common dung-worm).
OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
OC Lumbricina; Lumbricidae; Eisenia.
OX NCBI_TaxID=6396;
RN [1]
RP SEQUENCE.
RX TISSUE=Pituitary;
RX MEDLINE=94121660; PubMed=8292046;
RA Oumi T., Ukena K., Matsushima O., Ikeda T., Fujita T., Minakata H.,
RA Nomoto K.;
RT "Annetocin: an oxytocin-related peptide isolated from the earthworm, Eisenia foetida.";
RL Biochem. Biophys. Res. Commun. 198:393-399(1994).
CC -!- FUNCTION: POTENTIATES SPONTANEOUS CONTRACTIONS OF THE GUT AND ALSO PULSATORY CONTRACTIONS AND BLADDER-SHAKING MOVEMENT OF THE NEPHRIDIA. MAY BE INVOLVED IN OSMOREGULATION OF THE ANIMAL THROUGH NEPHRIDIAL FUNCTION.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR PIR: PC2021; PC2021.
DR InterPro: IPR000981; Neurhyp_horm.
DR Pfam: PF00220; hormone4; 1.
DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; FALSE_NEG.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
FT SEQUENCE 9 AA; 996 MW; DA4EB76EB45412C9 CRC64;

Query Match 20.2%; Score 18; DB 1; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 9 QGCPS 13
|| :||
Db 4 RNCPT 8

RESULT 11
PGLR_DIAAB PGLR_DIAAB STANDARD; PRT; 9 AA..
AC P81179;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Endo-polygalacturonase (PG) (EC 3.2.1.15) (Fragment).
OS Diaprepes abbreviatus (Sugarcane rootstalk borer weevil).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
OC Cucujiformia; Phytophaga; Curculionidae; Entiminae; Entimini;
OC Diaprepes.
OX NCBI_TaxID=13040;
RN [1]
RP SEQUENCE.
RX TISSUE=Larval gut;
RA Doostdar H., McCollum T.G., Mayer R.T.;
RT "Purification and characterization of an endo-polygalacturonase from the gut of West Indies sugarcane rootstalk borer weevil (Diaprepes abbreviatus L.) larvae.";
RL Comp. Biochem. Physiol. 118B:861-867(1997).
CC -!- CATALYTIC ACTIVITY: Random Hydrolysis of 1,4-alpha-D-galactosiduronic linkages in pectate and other galacturonans.
CC -!- INDUCTION: INHIBITED BY CITRUS PGIP.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS: 9.4, ITS MW IS: 44.5 kDa.
CC -!- SIMILARITY: WEAK, TO OTHER POLYGALACTURONASES.
KW Hydrolase; Glycosidase; Cell wall.

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FT NON_TER 9 9 1041 MW; 1F49087042DB41BB CRC64;
SQ SEQUENCE 9 AA; 20.2%; Score 18; DB 1; Length 9;
Query Match 37.5%; Pred. No. 1.1e+05;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YSOVLFGK 8
   | : |
Db 2 YTVVIGRG 9

RESULT 12
BPP_VIPAS STANDARD; PRT; 10 AA.
AC P31351;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Bradykinin-potentiating peptide (Angiotensin-converting
DE enzyme inhibitor).
OS Vipera aspis (Aspic viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Viperinae; Vipera.
OX NCBI_TaxID=8706;
RN [1]
RP SEQUENCE.
RC TISSUE-Venom;
RX MEDLINE=90382616; PubMed=2169439;
RA Komori Y., Sugihara H.;
RT "Characterization of a new inhibitor for angiotensin converting
RT enzyme from the venom of Vipera aspis aspis.";
RL Int. J. Biochem. 22:767-771(1990).
CC -!- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE
CC ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF
CC BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
CC IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
DR PIR: A60377; XASNPC.
KW Hypotensive agent; Venom.
FT MOD_RES 1 1
SQ SEQUENCE 10 AA; 1062 MW; 3BA827C327686773 CRC64;

Query Match 20.2%; Score 18; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 3.3e+03;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 9 QGCPSTHV 16
   | | | |
Db 1 QGWPGPKV 8

RESULT 13
H2AX_ONCMY STANDARD; PRT; 12 AA.
AC P83327;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Histone H2A (Fragment).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE-Skin mucus;
RA Fernandes J.M.O., Kemp G.D., Molle G., Smith V.J.;
RT "Antimicrobial properties of a histone H2A-like protein from skin
RT secretions of rainbow trout, Oncorhynchus mykiss.";
RL Submitted (APR-2002) to the SWISS-PROT data bank.
CC -!- FUNCTION: Has antibacterial activity against Gram-positive
```

```
CC bacteria and antifungal activity against S.cerevisiae.
CC -!- SUBUNIT: The nucleosome is an octamer containing two molecules of
CC H2A, H2B, H3, and H4; which wrap approximately 146 bp of DNA.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- MASS SPECTROMETRY: MW=13639; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE HISTONE H2A FAMILY.
DR InterPro: IPR002119; Histone_H2A.
DR PROSITE: PS00046; HISTONE_H2A; PARTIAL.
KW Chromosomal protein; Nucleosome core; Nuclear protein;
KW DNA-binding; Antibiotic; Fungicide; Acetylation.
FT NON_TER 1 1
FT MOD_RES 12 12
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1202 MW; 3EF28D9668D87DD8 CRC64;

Query Match 20.2%; Score 18; DB 1; Length 12;
Best Local Similarity 60.0%; Pred. No. 3.9e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 GQGCP 12
   | | |
Db 5 GAGAP 9

RESULT 14
CXA2_CONMA STANDARD; PRT; 16 AA.
AC P56636;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Alpha-conotoxin MII (M2).
OS Conus magus (Magus cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6492;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE-Venom;
RX MEDLINE=96205934; PubMed=8631783;
RA Cartier G.E., Yoshikami D., Gray W.R., Luo S., Olivera B.M.,
RA McIntosh J.M.;
RT "A new alpha-conotoxin which targets alpha3beta2 nicotinic
RT acetylcholine receptors.";
RL J. Biol. Chem. 271:7522-7528(1996).
RN [2]
RP STRUCTURE BY NMR.
RX MEDLINE=98062282; PubMed=9398298;
RA Shon K.-J., Koerber S.C., Rivier J.E., Olivera B.M., McIntosh J.M.;
RT "Three-dimensional solution structure of alpha-conotoxin MII, an
RT alpha3beta2 neuronal nicotinic acetylcholine receptor-targeted
RT ligand.";
RL Biochemistry 36:15693-15700(1997).
RN [3]
RP STRUCTURE BY NMR.
RX MEDLINE=99060038; PubMed=9843366;
RA Hill J.M., Oomen C.J., Miranda L.P., Bingham J.-P., Alewood P.F.,
RA Craik D.J.;
RT "Three-dimensional solution structure of alpha-conotoxin MII by NMR
RT spectroscopy: effects of solution environment on helicity.";
RL Biochemistry 37:15621-15630(1998).
CC -!- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
CC INHIBIT THEM. THIS PEPTIDE BLOCKS MAMMALIAN NICOTINIC
CC ACETYLCHOLINE RECEPTORS COMPOSED OF ALPHA-3/BETA-2 SUBUNITS. IT
CC HAS AN ACTIVITY 2 TO 4 ORDERS OF MAGNITUDE LESS POTENT ON OTHER
CC NACHR SUBUNIT COMBINATIONS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
CC FAMILY.
DR PDB: 1MII; 21-OCT-98.
DR PDB: 1M2C; 13-JAN-99.
```

KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
 KW Acetylcholine receptor inhibitor; Amidation; 3D-structure.
 FT DISULFID 2 8
 FT DISULFID 3 16
 FT MOD_RES 16 16
 SQ SEQUENCE 16 AA; 1716 MW; 282AEF190166CAF9 CRC64;
 AMIDATION.

Query Match 20.2%; Score 18; DB 1; Length 16;
 Best Local Similarity 57.1%; Pred. No. 5.1e+03;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 10 GCPSTHV 16
 |||||
 Db 1 GCCSNPV 7

RESULT 15

CONO_CONGE STANDARD; PRT; 9 AA.
 AC P05486;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lys-conopressin G.
 OS Conus geographus (Geography cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=6491;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=88058932; PubMed=3680228;
 RA Cruz L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D.,
 RA Gray W.R., Olivera B.M.;
 RT "Invertebrate vasopressin/oxytocin homologs. Characterization of
 RT peptides from Conus geographus and Conus straitus venoms.";
 RL J. Biol. Chem. 262:15821-15824(1987).
 RN [2]
 RP REVIEW.
 RX MEDLINE=89024586; PubMed=3052286;
 RA Gray W.R., Olivera B.M., Cruz L.J.;
 RT "Peptide toxins from venomous Conus snails.";
 RL Annu. Rev. Biochem. 57:665-700(1988).
 CC -|- SURCELLULAR LOCATION: Secreted.
 CC -|- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
 DR PIR; A28495; A28495.
 DR InterPro; IPR000981; Neurohyp_horm.
 DR Pfam; PF00220; hormone4; 1.
 DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
 KW Hormone; Amidation.
 FT DISULFID 1 6
 FT MOD_RES 9 9
 SQ SEQUENCE 9 AA; 1037 MW; D4FC276EB4540059 CRC64;
 AMIDATION.

Query Match 19.1%; Score 17; DB 1; Length 9;
 Best Local Similarity 50.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 9 QGCP 12
 :||
 Db 4 RNCP 7

Search completed: December 4, 2002, 13:31:33
 Job time : 11 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 4, 2002, 13:29:53 ; Search time 29 seconds
(without alignments)
113.681 Million cell updates/sec

Title: US-09-754-004-1

Perfect score: 89

Sequence: 1 YSQVLFGKGCPSSTHV 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 3565

Minimum DB seq length: 0

Maximum DB seq length: 16

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	29	32.6	16	Q9UD46	Q9ud46 homo sapien
2	28	31.5	15	Q9UCB9	Q9ucb9 homo sapien
3	28	31.5	16	Q9UD47	Q9ud47 homo sapien
4	26	29.2	16	Q9UD45	Q9ud45 homo sapien
5	26	29.2	16	Q9PR24	Q9pr24 bothrops ja
6	24	27.0	15	Q9R569	Q9r569 nitrosomona
7	24	27.0	15	Q62531	Q62531 mus spretus
8	24	27.0	16	Q16033	Q16033 homo sapien
9	23	25.8	10	Q8UVW2	Q8uvw2 oreochromis
10	23	25.8	12	Q8UVW0	Q8uvw0 rana catesb
11	23	25.8	12	Q8UVV8	Q8uvv8 squalus aca
12	23	25.8	16	Q9PRY2	Q9pry2 petromyzon
13	22	24.7	13	Q9TQ08	Q9tq08 homo sapien
14	22	24.7	13	Q9T201	Q9t201 bos taurus
15	22	24.7	14	Q43905	Q43905 azospirillum
16	22	24.7	14	P82219	P82219 bombyx mori

17	22	24.7	15	6	Q9TQ05	Q9tq05 bos taurus
18	21	23.6	9	11	O08979	O08979 mus musculus
19	21	23.6	10	11	O0QVF7	Q9qv7 rattus sp.
20	21	23.6	11	2	O8RM18	O8rm18 enterococcu
21	21	23.6	11	11	Q99JC3	Q99jc3 rattus sp.
22	21	23.6	11	13	Q9PS22	Q9ps22 xenopus lae
23	21	23.6	14	10	P82322	P82322 pisum sativ
24	21	23.6	14	12	P87540	P87540 barley mild
25	21	23.6	14	15	O88400	O88400 simian t-ly
26	21	23.6	15	1	Q9UWG1	Q9uwg1 pyrococcus,
27	21	23.6	15	2	Q9R5A1	Q9r5a1 micrococcus
28	21	23.6	15	4	Q9UC85	Q9uc85 homo sapien
29	21	23.6	15	12	Q9PXC5	Q9pxc5 tobacco etc
30	21	23.6	16	4	Q9UCR2	Q9ucr2 homo sapien
31	21	23.6	16	4	Q9UDE9	Q9ude9 homo sapien
32	21	23.6	16	8	Q95AY0	Q95ay0 artemisia r
33	21	23.6	16	12	P90290	P90290 barley mild
34	21	23.6	16	13	Q9PRU6	Q9pru6 gallus gall
35	20	22.5	9	12	P90359	P90359 barley mild
36	20	22.5	12	10	Q02319	Q02319 pinus sylve
37	20	22.5	12	10	Q38715	Q38715 arachis hyp
38	20	22.5	12	10	Q945C3	Q945c3 cryptocodi
39	20	22.5	12	12	Q69232	Q69232 bovine herp
40	20	22.5	15	13	Q9PRZ9	Q9prz9 micropogoni
41	20	22.5	16	13	Q8QGA1	Q8qgal brachydanio
42	19	21.3	8	4	Q9Y4X6	Q9y4x6 homo sapien
43	19	21.3	10	6	Q95NB1	Q95nb1 eulemur ful
44	19	21.3	11	6	Q95NB6	Q95nb6 eulemur ful
45	19	21.3	11	6	Q95J20	Q95j20 eulemur ful

ALIGNMENTS

RESULT 1

Q9UD46 ID Q9UD46 PRELIMINARY; PRT; 16 AA.
AC Q9UD46;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Gamma-interferon (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95038487; PubMed=7951030;
RA Smirnova O.Iu., Tat'kov S.I., Petrenko V.A., Il'ichev A.A.,
RA Sandakhchiev L.S.;
RT "[Mutant human gamma-interferons with varied C-termini and their
RT properties].";
RL Dokl. Akad. Nauk 337:405-406(1994).
SQ SEQUENCE 16 AA; 1865 MW; 2CF6C0D78CD4ECCA CRC64;

Query Match 32.6%; Score 29; DB 4; Length 16;
Best Local Similarity 62.5%; Pred. No. 3e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQVLFGKQ 9
Db 5 SQMLFRGR 12
11:11:1:

RESULT 2

Q9UCB9 ID Q9UCB9 PRELIMINARY; PRT; 15 AA.
AC Q9UCB9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Insulin-like growth factor receptor alpha subunit (Fragment).

OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE.
RX	MEDLINE=94079895; PubMed=8257688;
RA	Kasuya J., Paz I.B., Maddux B.A., Goldfine I.D., Hefta S.A.,
RA	Fujita-Yamaguchi Y.;
RT	"Characterization of human placental insulin-like growth factor-
RT	I/insulin hybrid receptors by protein microsequencing and
RT	purification."
RL	Biochemistry 32:13531-13536(1993).
SQ	SEQUENCE 15 AA; 1701 MW; 898F4684F9BB4006 CRC64;
Query Match 31.5%; Score 28; DB 4; Length 15;	
Best Local Similarity 33.3%; Pred. No. 4.2e+02;	
Matches 4; Conservative 3; Mismatches 5; Indels 0; Gaps 0;	
Oy	5 LFKGGGCPSTHV 16
Dd	1 : 1 : :
Dd	2 LYPGEVCPGMDI 13
RESULT 3	
Q9UD47	PRELIMINARY; PRT; 16 AA.
ID	Q9UD47
AC	Q9UD47; 2000 (TREMBLrel. 13, Created)
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT	01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE	Gamma-interferon (Fragment).
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=95038487; PubMed=7951030;
RA	Smirnova O.Iu., Tat'kov S.I., Petrenko V.A., Il'ichev A.A.,
RA	Sandakhchiev L.S.;
RT	"[Mutant human gamma-interferons with varied C-termini and their
RT	properties].";
RL	Dokl. Akad. Nauk 337:405-406(1994).
SQ	SEQUENCE 16 AA; 1837 MW; 2CF6C0D620BA84CB CRC64;
Query Match 31.5%; Score 28; DB 4; Length 16;	
Best Local Similarity 71.4%; Pred. No. 4.5e+02;	
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	
Oy	2 SQVLFGK 8
Dd	:: :
Dd	5 SQMLFRG 11
RESULT 4	
Q9UD45	PRELIMINARY; PRT; 16 AA.
ID	Q9UD45
AC	Q9UD45;
DT	01-MAY-2000 (TREMBLrel. 13, Created)
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT	01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE	Gamma-interferon (Fragment).
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=95038487; PubMed=7951030;
RA	Smirnova O.Iu., Tat'kov S.I., Petrenko V.A., Il'ichev A.A.,
RA	Sandakhchiev L.S.;
RT	"[Mutant human gamma-interferons with varied C-termini and their

QY 7 KGQCPSTHV 16
| | |
Db 1 KEVGICDCHV 10

RESULT 7

Q62531 PRELIMINARY; PRT; 15 AA.
AC Q62531; 1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-1998 (TrEMBLrel. 12, Last annotation update)
DE Placental calcium-binding protein (18A2) (PEL98) (MTS1 protein)
DE (Metastatic cell protein) (Fragment).
GN MTS1.
OS Mus spretus (Western wild mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10096;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRET/EI;
RX MEDLINE=94319082; PubMed=8043949;
RA Ko M.S., Wang X., Horton J.H., Hagen M.D., Takahashi N., Maezaki Y.,
RA Nadeau J.H.;
RT "Genetic mapping of 40 cDNA clones on the mouse genome by PCR.";
RL Mamm. Genome 5:349-355(1994).
CC -1- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS, AND MORE
CC SPECIFICALLY TO S-100/CABP LIKE PROTEINS.
DR EMBL; U05696; AAA61936.1; -;
KW Calcium-binding; Placenta.
FT NON_TER 1
SQ SEQUENCE 15 AA; 1824 MW; 31EBEA50E3987741 CRC64;

Query Match 27.0%; Score 24; DB 11; Length 15;
Best Local Similarity 75.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 QGCP 12
| | |
Db 5 EGCP 8

RESULT 8

Q16033 PRELIMINARY; PRT; 16 AA.
AC Q16033;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Alpha 2 type I procollagen (Fragment).
GN COL1A2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93244831; PubMed=1301191;
RA Edwards M.J., Wenstrup R.J., Byers P.H., Cohn D.H.;
RT "Recurrence of lethal osteogenesis imperfecta due to parental
RT mosaicism for a mutation in the COL1A2 gene of type I collagen. The
RT mosaic parent exhibits phenotypic features of a mild form of the
RT disease.";
RL Hum. Mutat. 1:47-54(1992).
DR EMBL; S62614; AAB26423.1; -;
KW Collagen.
FT NON_TER 1
SQ SEQUENCE 16 AA; 1423 MW; 1475AAA225155656 CRC64;

Query Match 27.0%; Score 24; DB 4; Length 16;
Best Local Similarity 44.4%; Pred. No. 2.3e+03;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 8 GQGPCSTHV 16
| | |
Db 4 GPSCPAGEV 12

RESULT 9

Q8UUVW2 PRELIMINARY; PRT; 10 AA.
AC Q8UUVW2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE AMPA receptor subunit 2 alpha (Fragment).
GN GLUR2A.
OS Oreochromis mossambicus (Mozambique tilapia) (Tilapia mossambica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Labroidel;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8127;
RN [1]
RP SEQUENCE FROM N.A.
RA Kung S.-S., Chen C.-C., Chen Y.-C., Chen B.-Y., Lin W.-H., Chow W.-Y.;
RT "Q/R RNA editing of the AMPA receptor subunit GLUR2 transcript evolves
RT no later than the appearance of cartilaginous fishes.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF350050; AAL57192.1; -;
KW Receptor.
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1153 MW; 721A6ESAEB866C4 CRC64;

Query Match 25.8%; Score 23; DB 13; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.2e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 FKQGC 11
| | |
Db 1 FMRQC 6

RESULT 10

Q8UUVW0 PRELIMINARY; PRT; 12 AA.
AC Q8UUVW0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE AMPA receptor subunit 2 (Fragment).
GN GLUR2.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RA Kung S.-S., Chen C.-C., Chen Y.-C., Chen B.-Y., Lin W.-H., Chow W.-Y.;
RT "Q/R RNA editing of the AMPA receptor subunit GLUR2 transcript evolves
RT no later than the appearance of cartilaginous fishes.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF350052; AAL57194.1; -;
KW Receptor.
FT NON_TER 1
FT NON_TER 12
SQ SEQUENCE 12 AA; 1269 MW; DD1A28D235B866C6 CRC64;

Query Match 25.8%; Score 23; DB 13; Length 12;
Best Local Similarity 66.7%; Pred. No. 2.6e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 FKQGC 11
| | |

Db 3 FMOQGC 8

RESULT 11

Q8UVV8

ID Q8UVV8 PRELIMINARY; PRT; 12 AA.

AC Q8UVV8; 12 AA.

DT 01-MAR-2002 (TREMBLrel. 20, Created)

DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)

DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

DE AMPA receptor subunit 2 (Fragment).

GN GLUR2.

OS Squalus acanthias (Spiny dogfish).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;

OC Elasmobranchii; Squala; Squaloidei; Squalidae; Squalus.

OX NCBI_TaxID=7797;

RN [1]

RP SEQUENCE FROM N.A.

RA Kung S.-S., Chen C.-C., Chen Y.-C., Lin W.-H., Chow W.-Y.;

RT "Q/R RNA editing of the AMPA receptor subunit GLUR2 transcript evolves

RL no later than the appearance of cartilaginous fishes."

RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF350054; AAL57196.1; -

KW Receptor.

FT NON_TER 1

FT NON_TER 12

FT NON_TER 12

SQ SEQUENCE 12 AA; 1253 MW; DD1A3E0835B866C6 CRC64;

Query Match 25.8%; Score 23; DB 13; Length 12;

Best Local Similarity 66.7%; Pred. No. 2.6e+03;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 FMOQGC 11

Db 3 FMOQGC 8

RESULT 12

Q9PRV2

ID Q9PRV2 PRELIMINARY; PRT; 16 AA.

AC Q9PRV2; 16 AA.

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)

DE Lectin 30 kDa subunit (Fragment).

OS Petromyzon marinus (Sea lamprey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;

OC Petromyzontiformes; Petromyzontidae; Petromyzon.

OX NCBI_TaxID=7757;

RN [1]

RP SEQUENCE.

RX MEDLINE=94249896; PubMed=8192354;

RA Schluter S.F., Schroeder J., Wang E., Marchalonis J.J.;

RT "Recognition molecules and immunoglobulin domains in invertebrates."

RL Ann. N. Y. Acad. Sci. 712:74-81(1994).

SQ SEQUENCE 16 AA; 1728 MW; 3BBF03DDA185F446 CRC64;

Query Match 25.8%; Score 23; DB 13; Length 16;

Best Local Similarity 75.0%; Pred. No. 3.4e+03;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 QGCP 12

Db 5 KGCP 8

RESULT 13

Q9TN08

ID Q9TN08 PRELIMINARY; PRT; 13 AA.

AC Q9TN08; 13 AA.

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-JULY-2002 (TREMBLrel. 21, Last annotation update)

DE HLA-A2 associated peptide (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE.

RX MEDLINE=92212461; PubMed=1557127;

RA Wei M.L., Cresswell P.;

RT "HLA-A2 molecules in an antigen-processing mutant cell contain signal

RT sequence-derived peptides."

RL Nature 356:443-446(1992).

KW MHC.

FT NON_TER 1

FT NON_TER 13

FT NON_TER 13

SQ SEQUENCE 13 AA; 1355 MW; 3E111BA716EA1768 CRC64;

Query Match 24.7%; Score 22; DB 7; Length 13;

Best Local Similarity 80.0%; Pred. No. 4.2e+03;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLFKG 8

Db 1 VLFKG 5

RESULT 14

Q9T2U1

ID Q9T2U1 PRELIMINARY; PRT; 13 AA.

AC Q9T2U1; 13 AA.

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE NADH:ubiquinone oxidoreductase (Complex I) iron-sulfur protein

DE fraction 20 kDa polypeptide peptide T-9 (Fragment).

OS Bos taurus (Bovine).

OG Mitochondrion.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RP SEQUENCE.

RX MEDLINE=92138662; PubMed=1778979;

RA Masui R., Wakabayashi S., Matsubara H., Hatefi Y.;

RT "The amino acid sequence of the 9 kDa polypeptide and partial amino

RT acid sequence of the 20 kDa polypeptide of mitochondrial

RT NADH:ubiquinone oxidoreductase."

RL J. Biochem. 110:575-582(1991).

FT NON_TER 1

FT NON_TER 13

FT NON_TER 13

SQ SEQUENCE 13 AA; 1369 MW; 0E61A5EAB35FDB50 CRC64;

Query Match 24.7%; Score 22; DB 8; Length 13;

Best Local Similarity 100.0%; Pred. No. 4.2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GCP 12

Db 10 GCP 12

RESULT 15

Q43905

ID Q43905 PRELIMINARY; PRT; 14 AA.

AC Q43905; 14 AA.

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE Dinitrogenase reductase (Fragment).

OS Azospirillum brasilense

OC Bacteria; Proteobacteria; alpha subdivision; Rhodospirillaceae;

OC Azospirillum.

OX NCBI_TaxID=192;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SP7;
RX MEDLINE=92250433; PubMed=1577701;
RA Zhang Y., Burris R.H., Roberts G.P.;
RT "Cloning, sequencing, mutagenesis, and functional characterization of
RL drat and drag genes from *Azospirillum brasilense*.";
DR J. Bacteriol. 174:3364-3369(1992).
EMBL: M87319; AAA22182.1; -;
FT NON_TER 14
SQ SEQUENCE 14 AA; 1485 MW; D0F9B16263390219 CRC64;

Query Match 24.7%; Score 22; DB 2; Length 14;
Best Local Similarity 37.5%; Pred. No. 4.5e+03;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 VLFKGQGC 11
Db : 1: 11
5 IFFEKPGC 12

Search completed: December 4, 2002, 13:32:08
Job time : 30 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 4, 2002, 13:24:34 ; Search time 34 seconds
(without alignments)
62.706 Million cell updates/sec

Title: US-09-754-004-1

Perfect score: 89

Sequence: 1 YSOVLFKGGCGPSTHV 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 255767

Minimum DB seq length: 0

Maximum DB seq length: 16

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_101002.*
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22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	59	66.3	14	11	AA06782 Tumour necrosis fa
2	53	59.6	13	11	AA06787 Tumour necrosis fa
3	52	58.4	15	16	AA06787 h-TNF (54-68). Sy
4	49	55.1	12	11	AA06781 Tumour necrosis fa
5	49	55.1	12	11	AA06786 Tumour necrosis fa
6	49	55.1	13	11	AA06783 Tumour necrosis fa
7	49	55.1	13	11	AA06785 Tumour necrosis fa
8	45	50.6	12	11	AA06784 Tumour necrosis fa
9	40	44.9	8	11	AA05473 Tumour necrosis fa
10	37	41.6	12	18	AAW35497 TNF alpha peptide

11	35	39.3	13	5	AA040302	Gamma-interferon-r
12	34	38.2	13	19	AAW47898	Human tumour necro
13	33	37.1	14	22	AAW98602	Human peptide #187
14	32	36.0	12	23	AAU87888	PDZ domain binding
15	31	34.8	8	16	AAU07525	Chemotactic peptid
16	31	34.8	12	18	AAW32664	Human platelet gly
17	31	34.8	12	19	AAW71794	Novel human diago
18	31	34.8	14	22	ABG25396	Model human diagno
19	31	34.8	15	23	ABW77735	N-terminal of SR p
20	30	33.7	9	21	AA032359	HLA B403 binding
21	30	33.7	9	22	AAU69041	Human TADG-12 immu
22	30	33.7	11	20	AAU31887	Tumour necrosis fa
23	30	33.7	11	20	AAU06475	Tumour necrosis fa
24	30	33.7	11	21	AA018620	Conserved sequence
25	30	33.7	11	23	AB081654	TNF/Fas ligand fam
26	30	33.7	14	20	AAU08356	Cysteine noose lib
27	30	33.7	15	21	AAU93089	Transforming growt
28	29	32.6	8	10	AAU91659	Synthetic peptide
29	29	32.6	11	10	AAU91662	Synthetic peptide
30	29	32.6	12	18	AAW35775	Cucurbita maxima t
31	29	32.6	14	8	AAU70890	Sequence encoded b
32	29	32.6	15	21	AAU93088	Transforming growt
33	29	32.6	16	7	AAU61044	Peptide remaining
34	29	32.6	16	18	AAU92299	Tryptic peptide fr
35	29	32.6	16	18	AAW12711	Unglycosylated rec
36	29	32.6	16	19	AAW68595	Wild type human in
37	29	32.6	16	22	AAU73183	Protease binding s
38	29	32.6	16	22	AAU73184	Protease binding s
39	29	32.6	16	22	AAU73185	Protease binding s
40	29	32.6	16	23	AAU69609	Cell death protect
41	28	31.5	9	23	AAU75754	Peptide sequence o
42	28	31.5	10	22	AAU95737	Human complementar
43	28	31.5	11	16	AAU87682	h-TNF (70-80). Sy
44	28	31.5	11	16	AAU87683	h-TNF (70-80). anal
45	28	31.5	11	18	AAW35449	Cytokine derived p

ALIGNMENTS

RESULT 1		
AAAR06782	ID	AAAR06782 standard; protein; 14 AA.
XX	AC	AAAR06782;
XX	DT	23-OCT-1990 (first entry)
XX	DE	Tumour necrosis factor derived peptide.
XX	KW	Tumour necrosis factor; TNF; neoplastic disease; autoimmune
XX	KW	disease; infection; inflammation; transplant rejection.
XX	OS	Synthetic.
XX	PN	DE3841762-A.
XX	PD	13-JUN-1990.
XX	PF	12-DEC-1988; 88DE-3841762.
XX	PR	12-DEC-1988; 88DE-3841762.
XX	PA	(BADI) BASF AG.
XX	PI	Bohm HJ, Daum L, Haupt A, Schmied B, Walker N, Zechel
XX	DR	WPI; 1990-186578/25.
XX	PT	Peptide(s) derived from tumour necrosis factor (TNF) - useful
XX	PT	neoplastic and auto-immune disorders, infections, inflammation
XX	PT	transplant rejection reactions.

```
PS Example 9; Page 8; 13pp; German.
XX To residue L1 is attached Ac and to residue L14 NH2.
CC This peptide is an example of a highly generic sequence of the
CC formula X-A-B-Pro-E-Y
CC A= G, A or S;
CC B= C, Y or T;
CC E= S or P;
CC X= G-NH-CHM-CO, G-NH-CHM-CO-W, G-R-NH-CHM-CO or G-R-NH-CHM-CO-W;
CC Y= Z, NH-CHQ-COZ, V-NH-CHQ-COZ, NH-CHQ-CO-U-Z or V-NH-CHQ-CO-U-Z;
CC G= H or an amino protecting group;
CC Z= OH, NH2 or carboxy protecting group; or G and Z together are a
CC covalent bond or the gp. CO(CH2)2NH; a=1-12;
CC R, U, V and W= peptide chains of 1-4 naturally occurring alpha aminoacids;
CC M and Q= H, isopropyl, sec-butyl, phenyl, 1-hydroxy-ethyl, 3-indolyl- or
CC 4-imidazolyl-methyl or (CH2)2BT; b=1-6;
CC T= OH, MeO, MeS, isopropyl, phenyl (opt. 4-OH, substd), mercapto,
CC amino, carboxy, carbamoyl or guanidino; or
CC M and Q together are (CH2)2C-S-(CH2)2d, (CH2)2ECO NH-(CH2)2f or
CC (CH)2eNH CO(CH2)2gNH CO(CH2)2f; c and d=1-4; e and f=1-6; g=1-12.
CC The peptide is a low mol. wt. deriv. of TNF.
CC See also DE3841753-55, DE3841759, DE3841761-64, DE3841767-68.
XX
XX SQ Sequence 14 AA;
Query Match 66.3%; Score 59; DB 11; Length 14;
Best Local Similarity 91.7%; Pred. No. 0.024; 1; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 LFKGGQGPSTHV 16
DB 1 LFKGGQGPSTHV 12
RESULT 2
AAR06787
ID AAR06787 standard; protein; 13 AA.
XX
AC AAR06787;
XX
DT 23-OCT-1990 (first entry)
XX
DE Tumour necrosis factor derived peptide.
XX
KW Tumour necrosis factor; TNF; neoplastic disease; autoimmune
KW disease; infection; inflammation; transplant rejection; cyclic.
XX
OS Synthetic.
XX
PN DE3841762-A.
XX
PD 13-JUN-1990.
XX
PF 12-DEC-1988; 88DE-3841762.
XX
PR 12-DEC-1988; 88DE-3841762.
XX
PA (BADI ) BASF AG.
XX
PI Bohm HJ, Daum L, Haupt A, Schmied B, Walker N, Zechel JC;
XX
DR WPI; 1990-186578/25.
XX
PT Peptide(s) derived from tumour necrosis factor (TNF) - useful against
PT neoplastic and auto-immune disorders, infections, inflammations and
PT transplant rejection reactions.
XX
PS Example 53; Page 12; 13pp; German.
XX
CC This peptide is an example of a highly generic sequence of the
CC formula X-A-B-Pro-E-Y
CC A= G, A or S;
CC B= C, Y or T;
CC E= S or P;
CC X= G-NH-CHM-CO, G-NH-CHM-CO-W, G-R-NH-CHM-CO or G-R-NH-CHM-CO-W;
CC Y= Z, NH-CHQ-COZ, V-NH-CHQ-COZ, NH-CHQ-CO-U-Z or V-NH-CHQ-CO-U-Z;
CC G= H or an amino protecting group;
CC Z= OH, NH2 or carboxy protecting group; or G and Z together are a
CC covalent bond or the gp. CO(CH2)2NH; a=1-12;
CC R, U, V and W= peptide chains of 1-4 naturally occurring alpha aminoacids;
CC M and Q= H, isopropyl, sec-butyl, phenyl, 1-hydroxy-ethyl, 3-indolyl- or
CC 4-imidazolyl-methyl or (CH2)2BT; b=1-6;
CC T= OH, MeO, MeS, isopropyl, phenyl (opt. 4-OH, substd), mercapto,
CC amino, carboxy, carbamoyl or guanidino; or
CC M and Q together are (CH2)2C-S-(CH2)2d, (CH2)2ECO NH-(CH2)2f or
CC (CH)2eNH CO(CH2)2gNH CO(CH2)2f; c and d=1-4; e and f=1-6; g=1-12.
CC The peptide is a low mol. wt. deriv. of TNF.
CC See also DE3841753-55, DE3841759, DE3841761-64, DE3841767-68.
XX
XX SQ Sequence 13 AA;
Query Match 59.6%; Score 53; DB 11; Length 13;
Best Local Similarity 83.3%; Pred. No. 0.18; 2; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 5 LFKGGQGPSTHV 16
DB 1 LFKGGQGPSTHV 12
RESULT 3
AAR87687
ID AAR87687 standard; peptide; 15 AA.
XX
AC AAR87687;
XX
DT 10-MAY-1996 (first entry)
XX
DE h-TNF (54-68).
XX
KW TNF; tumour necrosis factor; neutrophil; superoxide; inflammation;
KW AIDS; cancer; rheumatoid arthritis; ARDS; cystic fibrosis;
KW tuberculosis; TB; Crohn's disease; sarcoidosis; leprosy; syphilis;
KW malaria; adult respiratory distress syndrome.
XX
OS Synthetic.
XX
PN AU9344664-A.
XX
PD 02-MAR-1995.
XX
PF 12-MAR-1991; 91AU-0074762.
XX
PR 12-MAR-1991; 91AU-0074762.
XX
PR 13-AUG-1993; 93AU-0044664.
XX
PA (PEPT-) PEPTIDE TECHNOLOGY LTD.
XX
PI Ferrante A, Rathjen DA, Widmer F;
XX
DR WPI; 1995-115742/16.
XX
PT Novel peptides which stimulate neutrophils - are fragments of
PT tumour necrosis factor
XX
PS Disclosure; Page 15; 51pp; English.
XX
CC New peptides are provided which prime neutrophils for superoxide
CC production and an enhanced respiratory burst following treatment
CC with N-formyl-L-methionine-L-leucyl-L-phenylalanine. The peptides are
CC described generically. They are fragments from the region of amino acids
CC 54 to 94 of human TNF, or analogues of such fragments. Their
CC neutrophil-stimulating activity can be used in the treatment of diseases
CC such as AIDS, cancer, rheumatoid arthritis, ARDS, cystic fibrosis,
CC tuberculosis, Crohn's disease, sarcoidosis, leprosy, syphilis and
CC malaria. The present sequence is one of 6 specific peptides having the
```

CC above activity and which fit the the generic formula.

XX Sequence 15 AA;

Query Match 58.4%; Score 52; DB 16; Length 15;

Best Local Similarity 100.0%; Pred. No. 0.3;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSQVLFKGG 10

Db 6 YSQVLFKGG 15

RESULT 4

AAR06781

ID AAR06781 standard; protein; 12 AA.

XX AAR06781;

DT 23-OCT-1990 (first entry)

DE Tumour necrosis factor derived peptide.

XX Tumour necrosis factor; TNF; neoplastic disease; autoimmune

KW disease; infection; inflammation; transplant rejection.

XX Synthetic.

XX DE3841762-A.

XX 13-JUN-1990.

XX 12-DEC-1988; 88DE-3841762.

XX 12-DEC-1988; 88DE-3841762.

XX (BADI) BASF AG.

PI Bohm HJ, Daum L, Haupt A, Schmied B, Walker N, Zechel JC;

DR WPI; 1990-186578/25.

XX Peptide(s) derived from tumour necrosis factor (TNF) - useful against
PT neoplastic and auto-immune disorders, infections, inflammations and
PT transplant rejection reactions.

PS Example 2; Page 7; 13pp; German.

XX To residue K1 is attached H and to residue L12 OH.

CC This peptide is an example of a highly generic sequence of the
CC formula X-A-B-Pro-E-Y

CC A= G, A or S;

CC E= S or P;

CC X= G-NH-CHM-CO, G-NH-CHM-CO-W, G-R-NH-CHM-CO or G-R-NH-CHM-CO-W;

CC Y= Z, NH-CHO-COZ, V-NH-CHO-COZ, NH-CHO-CO-U-Z or V-NH-CHO-CO-U-Z;

CC G= H or an amino protecting group;

CC Z= OH, NH2 or carboxy protecting group; or G and Z together are a
CC covalent bond or the gp. CO(CH2)2aNH; a=1-12;

CC R, U, V and W= peptide chains of 1-4 naturally occurring alpha aminoacids;

CC M and Q= H, isopropyl, sec-butyl, phenyl, 1-hydroxy-ethyl, 3-indolyl- or
CC 4-imidazolyl-methyl or (CH2)bf; b=1-6;

CC T= OH, MeO, MeS, isopropyl, phenyl (opt. 4-OH, substd), mercapto,
CC amino, carboxy, carbamoyl or guanidino; or

CC M and Q together are (CH2)c-S-S-(CH2)d, (CH2)eCO NH-(CH2)f or
CC (CH2)2aNH CO(CH2)gNH CO(CH2) f; c and d=1-4; e and f=1-6; g=1-12.

CC The peptide is a low mol. wt. deriv. of TNF.

CC See also DE3841753-55, DE3841759, DE3841761-64, DE3841767-68.

XX Sequence 12 AA;

Query Match

Best Local Similarity 55.1%; Score 49; DB 11; Length 12;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 KGOGCPSTHV 16

Db 1 KGOGTPSTHV 10

RESULT 5

AAR06786

ID AAR06786 standard; protein; 12 AA.

XX AAR06786;

XX 23-OCT-1990 (first entry)

DE Tumour necrosis factor derived peptide.

XX Tumour necrosis factor; TNF; neoplastic disease; autoimmune
KW disease; infection; inflammation; transplant rejection; cyclic.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 12..12

FT /label=OTHER

FT /note="Aoc"

XX DE3841762-A.

XX 13-JUN-1990.

XX 12-DEC-1988; 88DE-3841762.

XX 12-DEC-1988; 88DE-3841762.

XX (BADI) BASF AG.

PI Bohm HJ, Daum L, Haupt A, Schmied B, Walker N, Zechel JC;

DR WPI; 1990-186578/25.

XX Peptide(s) derived from tumour necrosis factor (TNF) - useful against
PT neoplastic and auto-immune disorders, infections, inflammations and
PT transplant rejection reactions.

PS Example 47; Page 11; 13pp; German.

CC This peptide is an example of a highly generic sequence of the
CC formula X-A-B-Pro-E-Y

CC A= G, A or S;

CC B= C, Y or T;

CC E= S or P;

CC X= G-NH-CHM-CO, G-NH-CHM-CO-W, G-R-NH-CHM-CO or G-R-NH-CHM-CO-W;

CC Y= Z, NH-CHO-COZ, V-NH-CHO-COZ, NH-CHO-CO-U-Z or V-NH-CHO-CO-U-Z;

CC G= H or an amino protecting group;

CC Z= OH, NH2 or carboxy protecting group; or G and Z together are a
CC covalent bond or the gp. CO(CH2)2aNH; a=1-12;

CC R, U, V and W= peptide chains of 1-4 naturally occurring alpha aminoacids;

CC M and Q= H, isopropyl, sec-butyl, phenyl, 1-hydroxy-ethyl, 3-indolyl- or
CC 4-imidazolyl-methyl or (CH2)bf; b=1-6;

CC T= OH, MeO, MeS, isopropyl, phenyl (opt. 4-OH, substd), mercapto,
CC amino, carboxy, carbamoyl or guanidino; or

CC M and Q together are (CH2)c-S-S-(CH2)d, (CH2)eCO NH-(CH2)f or
CC (CH2)2aNH CO(CH2)gNH CO(CH2) f; c and d=1-4; e and f=1-6; g=1-12.

CC The peptide is a low mol. wt. deriv. of TNF.

CC See also DE3841753-55, DE3841759, DE3841761-64, DE3841767-68.

XX Sequence 12 AA;

Query Match

Best Local Similarity 55.1%; Score 49; DB 11; Length 12;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 KGQGPCSTHV 16
 Db 1 KGQGPSTHV 10

RESULT 6
 AAR06783
 ID AAR06783 standard; protein; 13 AA.

XX AC AAR06783;
 XX DT 23-OCT-1990 (first entry)
 XX DE Tumour necrosis factor derived peptide.
 XX KW Tumour necrosis factor; TNF; neoplastic disease; autoimmune
 XX KW disease; infection; inflammation; transplant rejection.
 XX OS Synthetic.

XX FH Key Location/Qualifiers
 XX FT Disulfide-bond 1..13

XX PN DE3841762-A.
 XX PD 13-JUN-1990.

XX PF 12-DEC-1988; 88DE-3841762.
 XX PR 12-DEC-1988; 88DE-3841762.

XX PA (BADI) BASF AG.

XX PI Bohm HJ, Daum L, Haupt A, Schmied B, Walker N, Zechel JC;
 XX WPI; 1990-186578/25.

XX Peptide(s) derived from tumour necrosis factor (TNF) - useful against
 PT neoplastic and auto-immune disorders, infections, inflammations and
 PT transplant rejection reactions.

PS Example 12; Page 8; 13pp; German.

CC To residue C1 is attached Ac and to residue C13 NH2.

CC This peptide is an example of a highly generic sequence of the
 CC formula X-A-B-Pro-E-Y

CC A= G, A or S;

CC B= C, Y or T;

CC E= S or P;

CC X= G-NH-CHM-CO, G-NH-CHM-CO-W, G-R-NH-CHM-CO or G-R-NH-CHM-CO-W;
 CC Y= Z, NH-CHQ-COZ, V-NH-CHQ-COZ, NH-CHQ-CO-U-Z or V-NH-CHQ-CO-U-Z;

CC G= H or an amino protecting group;

CC Z= OH, NH2 or carboxy protecting group; or G and Z together are a
 CC covalent bond or the gp. CO(CH2)anH; a=1-12;

CC R, U, V and W= peptide chains of 1-4 naturally occurring alpha aminoacids;
 CC M and Q= H, isopropyl, sec-butyl, phenyl, 1-hydroxy-ethyl, 3-indolyl- or
 CC 4-imidazolyl-methyl or (CH2)bt; b=1-6;

CC T= OH, MeO, MeS, isopropyl, phenyl (opt. 4-OH, substd), mercapto,
 CC amino, carboxy, carbamoyl or guanidino; or

CC M and Q together are (CH2)c-S-S-(CH2)d, (CH2)eCO NH-(CH2)f or
 CC (CH2)2eNH CO(CH2)gNH CO(CH2) i; c and d=1-4; e and f=1-6; g=1-12.

CC The peptide is a low mol. wt. deriv. of TNF.

CC See also DE3841753-55, DE3841759, DE3841761-64, DE3841767-68.

XX Sequence 13 AA;

Query Match 55.1%; Score 49; DB 11; Length 13;
 Best Local Similarity 90.0%; Pred. No. 0.74;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 KGQGPCSTHV 16
 Db 2 KGQGPSTHV 11

RESULT 7

AAR06785
 ID AAR06785 standard; protein; 13 AA.

XX AC AAR06785;

XX DT 23-OCT-1990 (first entry)

XX DE Tumour necrosis factor derived peptide.

XX KW Tumour necrosis factor; TNF; neoplastic disease; autoimmune
 XX KW disease; infection; inflammation; transplant rejection.

XX OS Synthetic.

XX PN DE3841762-A.

XX PD 13-JUN-1990.

XX PF 12-DEC-1988; 88DE-3841762.

XX PR 12-DEC-1988; 88DE-3841762.

XX PA (BADI) BASF AG.

XX PI Bohm HJ, Daum L, Haupt A, Schmied B, Walker N, Zechel JC;
 XX WPI; 1990-186578/25.

XX Peptide(s) derived from tumour necrosis factor (TNF) - useful against
 PT neoplastic and auto-immune disorders, infections, inflammations and
 PT transplant rejection reactions.

PS Example 38; Page 10; 13pp; German.

CC To residue E1 is attached Ac and to residue K13 NH2.

CC Residues Glu1 and Lys13 together form a covalent bond.

CC This peptide is an example of a highly generic sequence of the
 CC formula X-A-B-Pro-E-Y

CC A= G, A or S;

CC B= C, Y or T;

CC E= S or P;

CC X= G-NH-CHM-CO, G-NH-CHM-CO-W, G-R-NH-CHM-CO or G-R-NH-CHM-CO-W;
 CC Y= Z, NH-CHQ-COZ, V-NH-CHQ-COZ, NH-CHQ-CO-U-Z or V-NH-CHQ-CO-U-Z;

CC G= H or an amino protecting group;

CC Z= OH, NH2 or carboxy protecting group; or G and Z together are a
 CC covalent bond or the gp. CO(CH2)anH; a=1-12;

CC R, U, V and W= peptide chains of 1-4 naturally occurring alpha aminoacids;
 CC M and Q= H, isopropyl, sec-butyl, phenyl, 1-hydroxy-ethyl, 3-indolyl- or
 CC 4-imidazolyl-methyl or (CH2)bt; b=1-6;

CC T= OH, MeO, MeS, isopropyl, phenyl (opt. 4-OH, substd), mercapto,
 CC amino, carboxy, carbamoyl or guanidino; or

CC M and Q together are (CH2)c-S-S-(CH2)d, (CH2)eCO NH-(CH2)f or
 CC (CH2)2eNH CO(CH2)gNH CO(CH2) i; c and d=1-4; e and f=1-6; g=1-12.

CC The peptide is a low mol. wt. deriv. of TNF.

CC See also DE3841753-55, DE3841759, DE3841761-64, DE3841767-68.

XX Sequence 13 AA;

Query Match 55.1%; Score 49; DB 11; Length 13;
 Best Local Similarity 90.0%; Pred. No. 0.74;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 KGQGPCSTHV 16
 Db 2 KGQGPSTHV 11

RESULT 8

AAR06784
 ID AAR06784 standard; protein; 12 AA.

```
XX AC AAR06784;
XX DT 23-OCT-1990 (first entry)
XX DE Tumour necrosis factor derived peptide.
XX KW Tumour necrosis factor; TNF; neoplastic disease; autoimmune
XX KW disease; infection; inflammation; transplant rejection.
XX OS Synthetic.
XX PN DE3841762-A.
XX PD 13-JUN-1990.
XX PF 12-DEC-1988; 88DE-3841762.
XX PR 12-DEC-1988; 88DE-3841762.
XX PA (BADI ) BASF AG.
XX FI Bohm HJ, Daum L, Haupt A, Schmied B, Walker N, Zechel JC;
XX WI; 1990-186578/25.
XX PT Peptide(s) derived from tumour necrosis factor (TNF) - useful against
XX PT neoplastic and auto-immune disorders, infections, inflammations and
XX PT transplant rejection reactions.
XX PS Example 37; Page 10; 13pp; German.
XX CC To residue G1 is attached Ac and to residue K12 NH2.
XX CC Residues Glu1 and Lys12 together form a covalent bond.
XX CC This peptide is an example of a highly generic sequence of the
XX CC formula X-A-B-Pro-E-Y
XX CC A= G, A or S;
XX CC B= C, Y or T;
XX CC E= S or P;
XX CC X= G-NH-CHM-CO, G-NH-CHM-CO-W, G-R-NH-CHM-CO or G-R-NH-CHM-CO-W;
XX CC Y= Z, NH-CHQ-COZ, V-NH-CHQ-COZ, NH-CHQ-CO-U-Z or V-NH-CHQ-CO-U-Z;
XX CC Z= OH, NH2 or amino protecting group;
XX CC G= H or an amino protecting group;
XX CC covalent bond or the gp. CO(CH2)2aNH; a=1-12;
XX CC R, U, V and W= peptide chains of 1-4 naturally occurring alpha aminoacids;
XX CC M and Q= H, isopropyl, sec-butyl, phenyl, 1-hydroxy-ethyl, 3-indolyl- or
XX CC 4-imidazolyl-methyl or (CH2)2Br; b=1-6;
XX CC T= OH, MeO, MeS, isopropyl, phenyl (opt. 4-OH, substd), mercapto,
XX CC amino, carboxy, carbamoyl or guanidino; or
XX CC M ans Q together are (CH2)c-S-S-(CH2)d, (CH2)eCO NH-(CH2)f or
XX CC (CH)2eNH CO(CH2)gNH CO(CH2) f; c and d=1-4; e and f=1-6; g=1-12.
XX CC The peptide is a low mol. wt. deriv. of TNF.
XX CC See also DE3841753-55, DE3841759, DE3841761-64, DE3841767-68.
XX SQ Sequence 12 AA;
Query Match 50.6%; Score 45; DB 11; Length 12;
Best Local Similarity 80.0%; Pred. No. 2.8;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 7 KGQGCPTSHV 16
DB 1 EQGCTPSTHV 10
:|||||
RESULT 9
AAR05473
ID AAR05473 standard; protein; 8 AA.
XX AC AAR05473;
XX DT 23-OCT-1990 (first entry)
XX OS Unidentified.
```

```
DE Tumour necrosis factor derived peptide.
XX KW Tumour necrosis factor; TNF; neoplastic disease; autoimmune
XX KW disease; infection; inflammation; transplant rejection.
XX OS Synthetic.
XX PN DE3841762-A.
XX PD 13-JUN-1990.
XX PF 12-DEC-1988; 88DE-3841762.
XX PR 12-DEC-1988; 88DE-3841762.
XX PA (BADI ) BASF AG.
XX FI Bohm HJ, Daum L, Haupt A, Schmied B, Walker N, Zechel JC;
XX WI; 1990-186578/25.
XX PT Peptide(s) derived from tumour necrosis factor (TNF) - useful against
XX PT neoplastic and auto-immune disorders, infections, inflammations and
XX PT transplant rejection reactions.
XX PS Example 1; Page 7; 13pp; German.
XX CC To residue G1 is attached Ac and to residue H8 NH2.
XX CC This peptide is an example of a highly generic sequence of the
XX CC formula X-A-B-Pro-E-Y
XX CC A= G, A or S;
XX CC B= C, Y or T;
XX CC E= S or P;
XX CC X= G-NH-CHM-CO, G-NH-CHM-CO-W, G-R-NH-CHM-CO or G-R-NH-CHM-CO-W;
XX CC Y= Z, NH-CHQ-COZ, V-NH-CHQ-COZ, NH-CHQ-CO-U-Z or V-NH-CHQ-CO-U-Z;
XX CC Z= OH, NH2 or amino protecting group;
XX CC G= H or an amino protecting group;
XX CC covalent bond or the gp. CO(CH2)2aNH; a=1-12;
XX CC R, U, V and W= peptide chains of 1-4 naturally occurring alpha aminoacids;
XX CC M and Q= H, isopropyl, sec-butyl, phenyl (opt. 4-OH, substd), mercapto,
XX CC T= OH, MeO, MeS, isopropyl, phenyl (opt. 4-OH, substd), mercapto,
XX CC amino, carboxy, carbamoyl or guanidino; or
XX CC M ans Q together are (CH2)c-S-S-(CH2)d, (CH2)eCO NH-(CH2)f or
XX CC (CH)2eNH CO(CH2)gNH CO(CH2) f; c and d=1-4; e and f=1-6; g=1-12.
XX CC The peptide is a low mol. wt. deriv. of TNF.
XX CC See also DE3841753-55, DE3841759, DE3841761-64, DE3841767-68.
XX SQ Sequence 8 AA;
Query Match 44.9%; Score 40; DB 11; Length 8;
Best Local Similarity 87.5%; Pred. No. 7.8e+05;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 8 GQGCPTSH 15
DB 1 GQCTPSTH 8
:|||||
RESULT 10
AAW35497
ID AAW35497 standard; peptide; 12 AA.
XX AC AAW35497;
XX DT 22-APR-1998 (first entry)
XX DE TNF alpha peptide from W09738011.
XX KW T-cell stimulatory peptide; immunogen; non-dendritic; carrier; tumour;
XX KW scaffold; inhibition; metastasis; wound healing; solid phase.
XX OS Unidentified.
```

XX PN WO9738011-A1.
 XX PD 16-OCT-1997.
 XX PF 03-APR-1997; 97WO-DE00146.
 XX PR 03-APR-1996; 96DK-0000398.
 XX PA (PEPR-) PEPRESEARCH AS.
 XX PI Heegaard PMH, Jakobsen PH;
 XX DR WPI; 1997-512645/47.
 XX PT Non-dendritic peptide carrier linked to a solid phase - useful as a
 PT diagnostic agent and as a scaffold for production of chemical
 PT derivatives
 XX PS Example 7; Page 99; 262pp; English.
 XX CC A non-dendritic peptide carrier (A) has been developed which is coupled
 CC through a linker to a solid phase, forming a complex of (A)-solid phase.
 CC where (A) comprises 10-50 amino acids capable of forming a secondary
 CC structure in a benign buffer after liberation from the solid phase, and
 CC further the (A)-solid phase complex comprises an immunogenic substance
 CC and/or an immune mediator coupled on (A). The present sequence
 CC represents a peptide used in an example from the present invention. An
 CC (A)-solid phase complex can be used as a scaffold for the production of
 CC chemical derivatives, characterised by covalently attaching molecules at
 CC attachment points. Alternatively (A) is used as a scaffold-peptide for
 CC the incorporation into an immunostimulating Complex (Iscom) resulting an
 CC (A)-Iscom complex which is used for the chemical coupling of antigenic
 CC substances in an aqueous solution by conjugation. (A) derivatised with
 CC one or more peptides having fibronectin-, laminin- or vitronectin-like
 CC binding activities can be used for the promotion of cell-attachment to
 CC plastic surfaces, in particular to inhibit tumour growth and metastasis,
 CC and for promotion of wound healing. Also a derivatised (A) can be used
 CC for the selection of specifically-binding aptamers or as a diagnostic
 CC agent. Such diagnostic-(A) molecules could be used to detect molecules
 CC derived from or indicative of pregnancy or of a disease, such as an
 CC infectious, autoimmune or cancerous disease.
 XX SQ Sequence 12 AA;
 Query Match 41.6%; Score 37; DB 18; Length 12;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 CPSTHV 16
 DB 1 CPSTHV 6
 RESULT 11
 AAP40302
 ID AAP40302 standard; Peptide; 13 AA.
 XX AC AAP40302;
 XX DT 07-JUL-1992 (first entry)
 XX DE Gamma-interferon-related peptide.
 XX KW IFN; antibody; antigen; haptene.
 XX OS Synthetic.
 XX PN JP59122446-A.
 XX PD 14-JUL-1984.
 XX PF 28-DEC-1982; 82JP-0228115.
 Query Match 41.6%; Score 37; DB 18; Length 12;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX PR 28-DEC-1982; 82JP-0228115.
 XX PA (SAKA) OTSUKA PHARM KK.
 XX DR WPI; 1984-210450/34.
 XX PT Peptide with partial amino acid sequence of gamma interferon - used
 PT to prepare specific antibody for gamma-interferon.
 XX PS Claim 1; Page 1; 11pp; Japanese.
 XX CC The N-terminal Tyr residue is optional. The peptide hapten can be
 CC bound to a carrier and used to prepare IFN-gamma-specific anti-
 CC bodies. It may also be used in radio- or enzyme immunoassays.
 CC See also AAP40301.
 XX SQ Sequence 13 AA;
 Query Match 39.3%; Score 35; DB 5; Length 13;
 Best Local Similarity 66.7%; Pred. No. 98;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 OY 1 YSQVLFKQ 9
 DB 1 YSQMLFQGR 9
 RESULT 12
 AAW47898
 ID AAW47898 standard; peptide; 13 AA.
 XX AC AAW47898;
 XX DT 09-JUN-1998 (first entry)
 XX DE Human tumour necrosis factor derived peptide 1089.
 XX KW Human; tumour necrosis factor; neutrophil; monocyte; macrophage;
 KW stimulatory activity; immunosuppressant; cancer; infection.
 XX OS Synthetic.
 XX OS Homo sapiens.
 XX PN WO9748725-A1.
 XX PD 24-DEC-1997.
 XX PF 20-JUN-1997; 97WO-AU000395.
 XX PR 29-OCT-1996; 96AU-0003309.
 XX PR 21-JUN-1996; 96AU-0000610.
 XX PR 06-SEP-1996; 96AU-0002165.
 XX PA (PEPT-) PEPTTECH LTD.
 XX PI Mack PO, Rathjen DA, Sleight JM, Wildmer F;
 XX DR WPI; 1998-063077/06.
 XX PT Tumour necrosis factor-derived peptide(s) having neutrophil and-or
 PT monocyte-macrophage stimulatory activity - used for treating e.g.
 XX PS infections, immunosuppression or cancers
 XX PS Claim 4; Page 44; 65pp; English.
 XX CC The present sequence represents a peptide derived from a human tumour
 CC necrosis factor peptide. The peptide can have neutrophil and/or
 CC monocyte/macrophage stimulatory activity. The peptide is derived from
 CC the sequence of tumour necrosis factor (TNF)-derived peptide 419
 CC (PSTHVLITHTI; see AU74762/91 and 44664/93). It can have improved
 CC properties such as increased potency, extended in vivo half life or,
 CC particularly, specificity of action. It can have neutrophil stimulatory

CC activity (class 1), equal neutrophil and monocyte/macrophage stimulatory
 CC activity (class 2), or preferentially enhanced monocyte/macrophage
 CC stimulatory activity (class 3). It can be used for the treatment or
 CC prevention of infections. In particular, it can be used for treating
 CC AIDS, cancer, diabetes, nosocomial infection, tuberculosis, cystic
 CC fibrosis, community acquired pneumonia, meningitis, Mycobacteria,
 CC Chlamydia, Brucellae, Francisella, Pasteurellosis, Legionellosis,
 CC Histoplasmosis, Listriosis, Pneumocystis carinii, Trypanosoma cruzi,
 CC coccidian parasitical infection, an inherited primary neutropenic
 CC disorder, an inherited defect of phagocytic cell function, an
 CC inherited secondary defect of phagocytic cell function, an acquired
 CC defect of phagocytic cell function, immunosuppression due to the
 CC administration of immunosuppressive drugs, and other bacterial, fungal,
 CC viral or protozoan infection, infectious mononucleosis, paroxysmal
 CC nocturnal, haemoglobinuria, leukaemia, lymphoma, myelofibrosis, or graft
 CC versus host disease.

XX
 SQ Sequence 13 AA;

Query Match 38.2%; Score 34; DB 19; Length 13;
 Best Local Similarity 85.7%; Pred. No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GCPSTHV 16
 | | | | |
 Db 1 GAPSTHV 7

RESULT 13
 AAM98602

ID AAM98602 standard; Peptide; 14 AA.

XX
 AC AAM98602;

DT 24-JAN-2002 (first entry)

DE Human peptide #1877 encoded by a SNP oligonucleotide.

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease.

XX Homo sapiens.

XX WO200147944-A2.

XX 05-JUL-2001.

PF 28-DEC-2000; 2000WO-US35498.

XX 28-DEC-1999; 99US-0173419.

PR 27-DEC-2000; 2000US-0173419.

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach M;

PI WPI; 2001-465210/50.

XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosing and treating, e.g.
 PT cancer, autoimmune diseases and infections -

XX Disclosure; Page 4079; 4143pp; English.

XX The present invention relates to oligonucleotides (see AAL26793-AAL34659)
 CC encoding polymorphic variants of proteins related to amylases, amyloid
 CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,

CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
 CC complement related proteins, cytochromes, kinesins, cytokines,
 CC interferons, interleukins, G-protein coupled receptors and thioesterases.
 CC The present sequence is a peptide encoded by one such oligonucleotide.
 CC The oligonucleotides and the peptides encoded by them may be used in the
 CC prevention, diagnosis and treatment of diseases associated with
 CC inappropriate expression of the proteins listed above. Disorders that may
 CC be prevented, diagnosed and/or treated include multifactorial diseases
 CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid
 CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus
 CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
 CC brain, breast, colon and kidney, leukaemia), diseases of the nervous
 CC system and an infection of pathogenic organisms.

SQ Sequence 14 AA;

Query Match 37.1%; Score 33; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CPSTH 15

Db 1 CPSTH 5

RESULT 14

AAU87888
 ID AAU87888 standard; Peptide; 12 AA.

XX
 AC AAU87888;

DT 05-JUN-2002 (first entry)

DE PDZ domain binding peptide #21.

XX Human; PDZ domain; WW domain; rat; cow; mouse; fruitfly; protein therapy;
 KW gene therapy; PDZ-mediated disease; inward potassium channel; WBP;
 KW dimer inhibitor peptide; carboxylate binding loop.

XX Homo sapiens.

XX WO200207751-A1.

PD 31-JAN-2002.

XX 24-JUL-2001; 2001WO-US23269.

XX 25-JUL-2000; 2000US-221215P.

PR 28-NOV-2000; 2000US-0723810.

XX (AXCE-) AXCELL BIOSCIENCES CORP.

XX Herrero J, Pirozzi G, Uveges A;

PI WPI; 2002-195842/25.

XX Methods for identifying polypeptides comprising PDZ domains, the
 PT polypeptides and their encoding nucleic acids, useful for the diagnosis
 PT and treatment of PDZ related disorders -

XX Examples; Fig 5; 225pp; English.

XX The invention relates to methods for identifying polypeptides comprising
 CC PDZ domains, and their encoding nucleic acids. The sequences are used to
 CC identify modulators of their expression, function and activity, for use
 CC in the diagnosis and treatment of PDZ related disorders. Antibodies
 CC against the proteins and cells that produce them may be used for the
 CC treatment of PDZ-mediated disease states. Sequences AAU87843-AAU87974
 CC represent proteins containing PDZ domains, fragments of these proteins
 CC and other related peptides used in the methods of the invention.

XX Sequence 12 AA;

Query Match 36.0%; Score 32; DB 23; Length 12;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 CPSTHV 16
||| ||
DB 5 CPSAHV 10

RESULT 15
AAV07525
ID AAV07525 standard; peptide; 8 AA.
XX
AC AAV07525;
XX
DT 17-AUG-1999 (first entry)
XX
DE Chemotactic peptide linked to metal-binding domain.
XX
KW Chemotactic; diagnostic; metal-binding; polyvalent; linked;
KW branched; repeat; neutrophil accumulation; infection; inflammation.
XX
OS Synthetic.

XX
FH Key Location/Qualifiers
FT Domain 1..4
FT /label= Biological_function
FT /note= "Chemotactic peptide"
FT Domain 5..8
FT /label= metal_ion-binding
FT Modified-site 1
FT /note= "N-formyl-Met"
FT Cross-links 4
FT /note= "This residue is joined to another
FT peptide of the same identity via a linking
FT group connecting the epsilon-COOH groups in each
FT of the Glu residues"

XX
PN W09501188-A1.
XX
PD 12-JAN-1995.
XX
PF 01-JUL-1994; 94WO-US07462.
XX
PR 30-JUN-1994; 94US-0269929.
PR 02-JUL-1993; 93US-0087219.
PR 20-FEB-1992; 92US-0840077.
PR 07-JUN-1995; 95US-0484184.
PR 09-AUG-1989; 89US-0391474.
PR 08-AUG-1990; 90US-0565275.
XX
PA (RHOM-) RHOMED INC.
XX
PI Zamora PO, Freer RJ, Rhodes BA, Sharma SD;
XX
DR WPI; 1995-060818/08.
XX
PT New high affinity peptide-based compsns. for diagnosis and therapy -
PT in which peptide has at least two biological-functional domains and
PT a metal ion binding domain
XX
PS Disclosure; Page 37; 60pp; English.
XX
CC The patent discloses a high affinity peptide-based pharmaceutical
CC composition which comprises (a) at least two linear repeat, linked or
CC branched amino acid sequence biological-function domains and (b) one
CC or more medically useful metal ion-binding domains. When bound with
CC a medically useful metal (e.g. an isotope of Tc, Re, In, Au, Ag, Hg
CC or Cu), the composition can be used for detection and treatment of
CC pathological conditions and for diagnostic imaging. The composition
CC allows direct binding with a metal without the necessity of
CC conjugation to bifunctional chelators. Metals can be bound while
CC retaining the high activity of the biological function domains.

CC The present sequence represents a chemotactic peptide (a preferred
CC example of a biological function domain) joined to a metal ion
CC binding domain. When bound with metal, this peptide can be used for
CC the detection of sites of neutrophil accumulation for the diagnosis
CC of infection and sterile inflammation.
XX
SQ Sequence 8 AA;
Query Match 34.8%; Score 31; DB 16; Length 8;
Best Local Similarity 62.5%; Pred. No. 7.8e+05;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 VLFKGGGC 11
:|:| |
DB 1 MLFEGGGC 8

Search completed: December 4, 2002, 13:31:16
Job time : 36 secs

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OM protein - protein search, using sw model

Run on: December 4, 2002, 13:32:14 ; Search time 10 seconds
(without alignments)
25.988 Million cell updates/sec

Title: US-09-754-004-1

Perfect score: 89

Sequence: 1 YSOVLFGQGCPTSHV 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 103943 seqs, 16242309 residues

Total number of hits satisfying chosen parameters: 28134

Minimum DB seq length: 0

Maximum DB seq length: 16

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB pep.*
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- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	89	100.0	16	10	US-09-754-004-1
2	30	33.7	11	10	US-09-027-287-46
3	30	33.7	11	10	US-09-252-656B-46
4	27	30.3	9	9	US-09-771-415-5
5	27	30.3	9	9	US-09-996-288-6
6	27	30.3	9	10	US-09-796-848A-7
7	27	30.3	10	9	US-09-984-245-291
8	26	29.2	11	10	US-09-253-794-39
9	26	29.2	15	9	US-09-826-290-149
10	26	29.2	15	9	US-09-826-290-159
11	26	29.2	15	9	US-09-826-290-163
12	26	29.2	16	10	US-09-916-940-85
13	26	29.2	16	10	US-09-916-940-97
14	25	28.1	9	9	US-10-106-487-36
15	24	27.0	8	10	US-09-158-120A-48
16	24	27.0	12	9	US-09-981-876-265
17	24	27.0	14	10	US-09-747-029A-16
18	24	27.0	15	10	US-09-965-594-8
19	24	27.0	15	10	US-09-965-594-9

20	24	27.0	15	10	US-09-965-594-10	Sequence 10, Appl
21	24	27.0	16	10	US-09-811-123-11	Sequence 11, Appl
22	23	25.8	8	10	US-09-794-927-62	Sequence 62, Appl
23	23	25.8	8	10	US-09-795-847-62	Sequence 62, Appl
24	23	25.8	8	10	US-09-794-743-62	Sequence 62, Appl
25	23	25.8	8	10	US-09-794-748-62	Sequence 62, Appl
26	23	25.8	8	10	US-09-794-925-62	Sequence 62, Appl
27	23	25.8	8	10	US-09-681-442-62	Sequence 62, Appl
28	23	25.8	9	8	US-08-854-825-26	Sequence 26, Appl
29	23	25.8	10	8	US-08-854-825-25	Sequence 25, Appl
30	23	25.8	10	9	US-10-117-476-6	Sequence 6, Appl
31	23	25.8	10	10	US-09-833-079-7	Sequence 7, Appl
32	23	25.8	11	9	US-09-826-290-102	Sequence 102, App
33	23	25.8	11	10	US-09-791-378-137	Sequence 137, App
34	23	25.8	12	9	US-09-981-876-267	Sequence 267, App
35	23	25.8	12	10	US-09-832-723-19	Sequence 19, Appl
36	23	25.8	12	10	US-09-375-924C-3	Sequence 3, Appl
37	22.5	25.3	12	9	US-09-758-426-55	Sequence 55, Appl
38	22.5	25.3	12	10	US-09-758-128-55	Sequence 55, Appl
39	22	24.7	7	12	US-10-066-151-9	Sequence 9, Appl
40	22	24.7	7	12	US-10-066-151-10	Sequence 10, Appl
41	22	24.7	8	12	US-10-095-450-9	Sequence 9, Appl
42	22	24.7	8	12	US-10-095-450-10	Sequence 10, Appl
43	22	24.7	8	12	US-10-066-151-14	Sequence 14, Appl
44	22	24.7	8	12	US-10-066-151-15	Sequence 15, Appl
45	22	24.7	9	9	US-09-835-948-95	Sequence 95, Appl

ALIGNMENTS

RESULT 1
US-09-754-004-1
; Sequence 1, Application US/09754004
; Patent No. US20020010180A1
; GENERAL INFORMATION:
; APPLICANT: Marc Feldmann
; TITLE OF INVENTION: TNF Alpha Antagonists and Methotrexate
; TITLE OF INVENTION: in the Treatment of TNF-Mediated Disease
; FILE REFERENCE: 2891.1001-026
; CURRENT APPLICATION NUMBER: US/09/754.004
; CURRENT FILING DATE: 2001-01-03
; PRIOR APPLICATION NUMBER: 08/690,775
; PRIOR FILING DATE: 1996-08-01
; PRIOR APPLICATION NUMBER: 08/607,419
; PRIOR FILING DATE: 1996-02-28
; PRIOR APPLICATION NUMBER: PCT/GB94/00462
; PRIOR FILING DATE: 1994-03-10
; PRIOR APPLICATION NUMBER: PCT/GB93/02070
; PRIOR FILING DATE: 1993-10-06
; PRIOR APPLICATION NUMBER: 07/958,248
; PRIOR FILING DATE: 1992-10-08
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-754-004-1

Query Match 100.0%; Score 89; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YSOVLFGQGCPTSHV 16

Db 1 YSOVLFGQGCPTSHV 16

RESULT 2

US-09-027-287-46

; Sequence 46, Application US/09027287A

; Patent No. US20020064869A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ruben, Steven M.
; APPLICANT: Ullrich, Stephen
; TITLE OF INVENTION: Apoptosis Inducing Molecule II
; FILE REFERENCE: 1488.0650004
; CURRENT APPLICATION NUMBER: US/09/027,287A
; CURRENT FILING DATE: 1998-02-20
; EARLIER APPLICATION NUMBER: US 09/003,886
; EARLIER FILING DATE: 1998-01-07
; EARLIER APPLICATION NUMBER: US 08/822,953
; EARLIER FILING DATE: 1997-03-21
; EARLIER APPLICATION NUMBER: US 60/030,157
; EARLIER FILING DATE: 1996-10-31
; EARLIER APPLICATION NUMBER: US 60/013,923
; EARLIER FILING DATE: 1996-03-22
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-027-287-46

Query Match 33.7%; Score 30; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSQVLF 6
| | | | |
Db 6 YSQVLF 11

RESULT 3

US-09-252-656B-46
; Sequence 46, Application US/09252656B
; Patent No. US20020081647A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ruben, Steven M.
; APPLICANT: Zhang, Jun
; APPLICANT: Ullrich, Stephen
; APPLICANT: Zhai, Yifan
; TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use
; FILE REFERENCE: 1488.0650006
; CURRENT APPLICATION NUMBER: US/09/252,656B
; CURRENT FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: US 60/075,409
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: US 09/027,287
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: US 09/003,886
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: US 08/822,953
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/013,923
; PRIOR FILING DATE: 1996-03-22
; PRIOR APPLICATION NUMBER: US 60/030,157
; PRIOR FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TNF/Fas Ligand Family Motif
US-09-252-656B-46

Query Match 33.7%; Score 30; DB 10; Length 11;

Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSQVLF 6
| | | | |
Db 6 YSQVLF 11

RESULT 4

US-09-771-415-5
; Sequence 5, Application US/09771415
; Patent No. US20020164326A1
; GENERAL INFORMATION:
; APPLICANT: Young, James F.
; APPLICANT: Koenig, Scott
; APPLICANT: Johnson, Leslie S.
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Ultra High Affinity Neutralizing Antibodies
; FILE REFERENCE: 469201-520
; CURRENT APPLICATION NUMBER: US/09/771,415
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,426
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Amino acid
; OTHER INFORMATION: sequence of complementarity determining region L3
; OTHER INFORMATION: of reference anti-RSV antibody
US-09-771-415-5

Query Match 30.3%; Score 27; DB 9; Length 9;
Best Local Similarity 55.6%; Pred. No. 8.6e+04;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 FKGGGCPST 14
| : | | | | |
Db 1 FQSGYPPT 9

RESULT 5

US-09-996-288-6
; Sequence 6, Application US/09996288
; Patent No. US20020171126A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophyl
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-6

Query Match 30.3%; Score 27; DB 9; Length 9;
Best Local Similarity 55.6%; Pred. No. 8.6e+04;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 FKGGGCPST 14
| : | | | | |

Db 1 FQSGYPPT 9

RESULT 6

US-09-796-848A-7

; Sequence 7, Application US/09796848A

; Patent No. US20020098189A1

; GENERAL INFORMATION:

; APPLICANT: Young, James F.

; APPLICANT: Johnson, Leslie S.

; APPLICANT: Huse, William D.

; APPLICANT: Wu, Herren

; APPLICANT: Watkins, Jeffery D.

; TITLE OF INVENTION: High Potency Recombinant Antibodies and Methods of

; FILE REFERENCE: 469201-526

; CURRENT APPLICATION NUMBER: US/09796,848A

; CURRENT FILING DATE: 2001-10-30

; PRIOR APPLICATION NUMBER: U.S. 60/186,252

; PRIOR FILING DATE: 2000-03-01

; NUMBER OF SEQ ID NOS: 59

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 7

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:Light chain

; OTHER INFORMATION: CDR reference sequence.

US-09-796-848A-7

Query Match

Best Local Similarity 30.3%; Score 27; DB 10; Length 9;

Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 6 FKGGGCPST 14

I I I I I

Db 1 FQSGYPPT 9

RESULT 7

US-09-984-245-291

; Sequence 291, Application US/09984245

; Patent No. US20020165374A1

; GENERAL INFORMATION:

; APPLICANT: Young et al.

; TITLE OF INVENTION: 87 Human Secreted Proteins

; FILE REFERENCE: P2004P1

; CURRENT APPLICATION NUMBER: US/09/984,245

; CURRENT FILING DATE: 2001-10-29

; PRIOR APPLICATION NUMBER: 09/154,707

; PRIOR FILING DATE: 1998-09-17

; PRIOR APPLICATION NUMBER: PCT/US98/05311

; PRIOR FILING DATE: 1998-03-19

; PRIOR APPLICATION NUMBER: US 60/041,277

; PRIOR FILING DATE: 1997-03-21

; PRIOR APPLICATION NUMBER: US 60/042,344

; PRIOR FILING DATE: 1997-03-21

; PRIOR APPLICATION NUMBER: US 60/041,276

; PRIOR FILING DATE: 1997-03-21

; PRIOR APPLICATION NUMBER: US 60/041,281

; PRIOR FILING DATE: 1997-03-21

; PRIOR APPLICATION NUMBER: US 60/048,094

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: US 60/048,350

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: US 60/048,188

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: US 60/048,135

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: US 60/050,937

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: US 60/048,187

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: US 60/048,099

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: US 60/048,352

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: US 60/048,186

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: US 60/048,069

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: US 60/048,095

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: US 60/048,131

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: US 60/048,096

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: US 60/048,355

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: US 60/048,160

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: US 60/048,351

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: US 60/048,154

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: US 60/054,804

; PRIOR FILING DATE: 1997-08-05

; PRIOR APPLICATION NUMBER: US 60/056,370

; PRIOR FILING DATE: 1997-08-19

; PRIOR APPLICATION NUMBER: US 60/060,862

; PRIOR FILING DATE: 1997-10-02

; NUMBER OF SEQ ID NOS: 343

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 291

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-984-245-291

Query Match 30.3%; Score 27; DB 9; Length 10;

Best Local Similarity 100.0%; Pred. No. 79;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 QGCP 12

I I I I I

Db 2 QGCP 5

RESULT 8

US-09-253-794-39

; Sequence 39, Application US/09253794

; Patent No. US20020018750A1

; GENERAL INFORMATION:

; APPLICANT: HANSEN, Hans J.

; TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED

; NUMBER OF SEQUENCES: 58

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: 3000 K Street, N.W., Suite 500

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20007-5109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/253,794

; FILING DATE: 22-Feb-1999

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

```
; APPLICATION NUMBER: US 08/318,157
; FILING DATE: 05-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 18733/464
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-253-794-39

Query Match      29.2%; Score 26; DB 10; Length 11;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      8 GGGCPST 14
        |||||
Db       2 GGGTPVT 8

RESULT 9
US-09-826-290-149
; Sequence 149, Application US/09826290
; Patent No. US20020164668A1
; GENERAL INFORMATION:
; APPLICANT: Durham, L. Kathryn
; APPLICANT: Friedmann, David L.
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
; APPLICANT: Kimmel, Lida H.
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Potter, David M.
; APPLICANT: Rohlf, Christian
; APPLICANT: Silber, B. Michael
; APPLICANT: Stiger, Thomas R.
; APPLICANT: Sunderland, P. Trey
; APPLICANT: Townsend, Robert Reid
; APPLICANT: White, Frost
; APPLICANT: Williams, Stephen A.
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and
; TITLE OF INVENTION: Uses Therefor, Including Diagnosis and Treatment of
; FILE REFERENCE: 2572-1-001 N2
; CURRENT APPLICATION NUMBER: US/09/826,290
; PRIOR FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/194,504
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 60/253,647
; NUMBER OF SEQ ID NOS: 492
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 159
; LENGTH: 15
; TYPE: PRT
; ORGANISM: homo sapien
US-09-826-290-159

Query Match      29.2%; Score 26; DB 9; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      6 FKGGCC 11
        | | | | |
Db       4 FFGGCC 9

RESULT 11
US-09-826-290-163
; Sequence 163, Application US/09826290
; Patent No. US20020164668A1
; GENERAL INFORMATION:
; APPLICANT: Durham, L. Kathryn
; APPLICANT: Friedmann, David L.
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
; APPLICANT: Kimmel, Lida H.
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Potter, David M.
; APPLICANT: Rohlf, Christian
; APPLICANT: Silber, B. Michael
; APPLICANT: Stiger, Thomas R.
; APPLICANT: Sunderland, P. Trey
; APPLICANT: Townsend, Robert Reid
; APPLICANT: White, Frost
; APPLICANT: Williams, Stephen A.
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and
; TITLE OF INVENTION: Uses Therefor, Including Diagnosis and Treatment of
; FILE REFERENCE: 2572-1-001 N2
; CURRENT APPLICATION NUMBER: US/09/826,290
; PRIOR FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/194,504
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 60/253,647
; NUMBER OF SEQ ID NOS: 492
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 149
; LENGTH: 15
; TYPE: PRT
; ORGANISM: homo sapien
US-09-826-290-149

Query Match      29.2%; Score 26; DB 9; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      6 FKGGCC 11
        | | | | |
Db       4 FFGGCC 9
```

; PRIOR FILING DATE: 2000-11-28
 ; NUMBER OF SEQ ID NOS: 492
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 163
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: homo sapien
 US-09-826-290-163

Query Match 29.2%; Score 26; DB 9; Length 15;
 Best Local Similarity 66.7%; Pred. No. 1.7e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 6 FKGGC 11
 | | : | |
 Db 4 FFGEC 9

RESULT 12

US-09-916-940-85
 ; Sequence 85, Application US/09916940
 ; Patent No. US20020127564A1

GENERAL INFORMATION:

; APPLICANT: No. US20020127564Alan, Garry P
 ; TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT INTRACELLULAR
 ; FILE REFERENCE: A-64260-6/RMS/AMS
 ; CURRENT APPLICATION NUMBER: US/09/916,940
 ; CURRENT FILING DATE: 2001-07-27
 ; PRIOR APPLICATION NUMBER: US 09/727,715
 ; PRIOR FILING DATE: 2000-11-28
 ; PRIOR APPLICATION NUMBER: US 08/963,368
 ; PRIOR FILING DATE: 1997-11-03
 ; PRIOR APPLICATION NUMBER: US 08/589,109
 ; PRIOR FILING DATE: 1996-01-23
 ; PRIOR APPLICATION NUMBER: US 08/589,911
 ; PRIOR FILING DATE: 1996-01-23
 ; PRIOR APPLICATION NUMBER: US 08/789,333
 ; PRIOR FILING DATE: 1997-01-23
 ; PRIOR APPLICATION NUMBER: US 08/787,738
 ; PRIOR FILING DATE: 1997-01-23
 ; NUMBER OF SEQ ID NOS: 102
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 85
 ; LENGTH: 16
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 US-09-916-940-85

Query Match 29.2%; Score 26; DB 10; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GCPS 13
 | | | | |
 Db 2 GCPS 5

RESULT 13

US-09-916-940-97
 ; Sequence 97, Application US/09916940
 ; Patent No. US20020127564A1

GENERAL INFORMATION:

; APPLICANT: No. US20020127564Alan, Garry P
 ; TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT INTRACELLULAR
 ; FILE REFERENCE: A-64260-6/RMS/AMS
 ; CURRENT APPLICATION NUMBER: US/09/916,940
 ; CURRENT FILING DATE: 2001-07-27
 ; PRIOR APPLICATION NUMBER: US 09/727,715
 ; PRIOR FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: US 08/963,368
 ; PRIOR FILING DATE: 1997-11-03
 ; PRIOR APPLICATION NUMBER: US 08/589,109
 ; PRIOR FILING DATE: 1996-01-23
 ; PRIOR APPLICATION NUMBER: US 08/589,911
 ; PRIOR FILING DATE: 1996-01-23
 ; PRIOR APPLICATION NUMBER: US 08/789,333
 ; PRIOR FILING DATE: 1997-01-23
 ; PRIOR APPLICATION NUMBER: US 08/787,738
 ; PRIOR FILING DATE: 1997-01-23
 ; NUMBER OF SEQ ID NOS: 102
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 97
 ; LENGTH: 16
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 US-09-916-940-97

Query Match 29.2%; Score 26; DB 10; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GCPS 13
 | | | | |
 Db 2 GCPS 5

RESULT 14

US-10-106-487-36
 ; Sequence 36, Application US/10106487
 ; Patent No. US20020164721A1

GENERAL INFORMATION:

; APPLICANT: FIRAT, HUSEYIN
 ; APPLICANT: LEMONNIER, FRANCOIS
 ; APPLICANT: LANGLADE-DEMOYEN, PIERRE
 ; APPLICANT: MICHEL, MARIE-LOUISE
 ; TITLE OF INVENTION: DESIGN OF A POLYPEPTIDIC CONSTRUCT FOR THE INDUCTION
 ; TITLE OF INVENTION: OF
 ; TITLE OF INVENTION: HLA-A2.1 RESTRICTED HIV 1 SPECIFIC CTL RESPONSES USING
 ; FILE REFERENCE: 03495.0196 SEQUENCE LISTING
 ; CURRENT APPLICATION NUMBER: US/10/106,487
 ; CURRENT FILING DATE: 2002-03-27
 ; PRIOR APPLICATION NUMBER: 09/675,673
 ; PRIOR FILING DATE: 2000-09-29
 ; PRIOR APPLICATION NUMBER: 60/158,356
 ; PRIOR FILING DATE: 1999-10-12
 ; NUMBER OF SEQ ID NOS: 41
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 36
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Human immunodeficiency virus type 1
 ; FEATURE:
 ; NAME/KEY: VARIANT
 ; LOCATION: (9)
 ; OTHER INFORMATION: L9V MUTANT EPITOPE
 US-10-106-487-36

Query Match 28.1%; Score 25; DB 9; Length 9;
 Best Local Similarity 57.1%; Pred. No. 8.6e+04;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VLFKGG 10
 : | : | : |
 Db 1 LLWKEG 7

RESULT 15

US-09-158-120A-48
 ; Sequence 48, Application US/09158120A

; Patent No. US2002010257A1
; GENERAL INFORMATION:
; APPLICANT: JOHNSON, L.
; TITLE OF INVENTION: Human Murine Chimeric Antibodies Against
; TITLE OF INVENTION: Respiratory Syncytial Virus
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
; ADDRESSEE: STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: P160
; OPERATING SYSTEM: Windows95
; SOFTWARE: MS Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/158,120A
; FILING DATE: September 21, 1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/290,592
; FILING DATE: August 15, 1994
; APPLICATION NUMBER: 07/813,372
; FILING DATE: December 23, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 469201-367
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 973-994-1700
; TELEFAX: 973-994-1744
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 AMINO ACIDS
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; US-09-158-120A-48

Query Match 27.0%; Score 24; DB 10; Length 8;
Best Local Similarity 57.1%; Pred. No. 8.6e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 6 FKQGCPC 12
|:| | |
Db 1 FQSGGYP 7

Search completed: December 4, 2002, 13:35:48
Job time : 10 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 4, 2002, 13:30:39 ; Search time 14 Seconds
(without alignments)
33.626 Million cell updates/sec

Title: US-09-754-004-1

Perfect score: 89

Sequence: 1 YSQLFRKGQCPSTHV 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 116189

Minimum DB seq length: 0

Maximum DB seq length: 16

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA.*

1: /cgn2.6/ptodata/1/1aa/5A_COMB.pep.*

2: /cgn2.6/ptodata/1/1aa/5B_COMB.pep.*

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6: /cgn2.6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	59	66.3	15	1	US-08-107-235-19
2	59	66.3	15	3	US-08-714-960B-19
3	59	66.3	15	4	US-09-598-784-19
4	52	58.4	15	1	US-08-107-235-10
5	52	58.4	15	1	US-08-178-268-44
6	52	58.4	15	3	US-08-714-960B-10
7	52	58.4	15	4	US-09-598-784-10
8	35	39.3	16	4	US-09-157-864-7
9	31	34.8	12	2	US-08-406-330-43
10	31	34.8	12	2	US-08-556-597-43
11	30	33.7	9	4	US-09-518-046-143
12	29	32.6	10	2	US-08-253-678A-19
13	29	32.6	10	3	US-08-582-134B-19
14	29	32.6	11	2	US-08-598-873-54
15	29	32.6	11	4	US-08-605-430-54
16	29	32.6	16	6	5278286-4
17	28	31.5	8	2	US-08-290-853-25
18	28	31.5	11	1	US-08-107-235-15
19	28	31.5	11	1	US-08-107-235-18
20	28	31.5	11	3	US-08-714-960B-15
21	28	31.5	11	3	US-08-714-960B-18
22	28	31.5	11	4	US-09-598-784-15
23	28	31.5	11	4	US-09-598-784-18
24	28	31.5	15	4	US-08-602-999A-345
25	28	31.5	15	4	US-09-500-124-345
26	28	31.5	16	5	PCT-US91-09422-29
27	27	30.3	15	2	US-08-945-168-99

28 27 30.3 15 3 US-09-035-749-3
29 26 29.2 9 1 US-08-615-181-108
30 26 29.2 9 4 US-09-518-046-125
31 26 29.2 11 2 US-08-318-157B-39
32 26 29.2 13 1 US-07-706-872-1
33 26 29.2 13 1 US-08-056-200-91
34 26 29.2 13 2 US-08-800-644-91
35 26 29.2 13 3 US-08-997-918-59
36 26 29.2 13 4 US-09-258-754-104
37 26 29.2 13 4 US-09-042-107-104
38 26 29.2 14 4 US-08-687-590-49
39 26 29.2 15 4 US-08-448-489-10
40 26 29.2 15 4 US-09-009-953-221
41 26 29.2 16 4 US-08-789-333F-85
42 26 29.2 16 4 US-08-789-333F-97
43 26 29.2 16 4 US-09-157-864-8
44 26 29.2 16 4 US-08-787-738B-85
45 26 29.2 16 4 US-08-787-738B-97

ALIGNMENTS

RESULT 1
US-08-107-235-19
; Sequence 19, Application US/08107235
; Patent No. 5587457
; GENERAL INFORMATION:
; APPLICANT: Rathjen, Deborah A
; APPLICANT: Ferrante, Antonio
; APPLICANT: Widmer, Fred
; TITLE OF INVENTION: Neutrophil Stimulating Peptides
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Allegretti & Witcoff, Ltd.
; STREET: 10 S. Wacker Dr.
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/107,235
; FILING DATE: 16-AUG-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,415
; FILING DATE: 12-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McDonnell, John J
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 92,622A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..15
; OTHER INFORMATION: /note= "PEPTIDE 462"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 5..6
; OTHER INFORMATION: /note= "CYS (ACM) PROTECTION

OTHER INFORMATION: PERMANENT"
US-08-107-235-19
Query Match 66.3%; Score 59; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 KGQGPCSTHV 16
Db 1 KGQGPCSTHV 10
RESULT 3
US-09-598-784-19
; Sequence 19, Application US/09598784
; Patent No. 6375928
; GENERAL INFORMATION:
; APPLICANT: RATHJEN, Deborah A
; TITLE OF INVENTION: Neutrophil Stimulating Peptides
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER & WITCOFF, LTD.
; STREET: 10 S. Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 Mb storage diskette, 3.50 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: IBM compatible PC/MS-DOS
; SOFTWARE: WordPerfect version 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/598,784
; FILING DATE: 21-Jun-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU RJ9065
; FILING DATE: 12-MAR-1990
; APPLICATION NUMBER: PCT/AU91/00086
; FILING DATE: 12-MAR-1991
; APPLICATION NUMBER: US 07/930,415
; FILING DATE: 09-NOV-1992
; APPLICATION NUMBER: US 08/107,235
; FILING DATE: 16-AUG-1993
; APPLICATION NUMBER: US 08/714,960
; FILING DATE: 17-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Resis, Robert H.
; REGISTRATION NUMBER: 32,168
; REFERENCE/DOCKET NUMBER: 11341.00001
; TELEPHONE: (312) 715-1000
; TELEFAX: (312) 715-1234
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 5..6
; OTHER INFORMATION: /product= "OTHER"
; /note= "CYS 5 (ACM) PROTECTION PERMANENT"
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..15
; OTHER INFORMATION: /note= "PEPTIDE 462"
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-598-784-19
Query Match 66.3%; Score 59; DB 4; Length 15;

OTHER INFORMATION: PERMANENT"
US-08-107-235-19
Query Match 66.3%; Score 59; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 KGQGPCSTHV 16
Db 1 KGQGPCSTHV 10
RESULT 2
US-08-714-960B-19
; Sequence 19, Application US/08714960B
; Patent No. 6121237
; GENERAL INFORMATION:
; APPLICANT: RATHJEN, Deborah A
; TITLE OF INVENTION: Neutrophil Stimulating Peptides
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER & WITCOFF, LTD.
; STREET: 10 S. Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 Mb storage diskette, 3.50 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: IBM compatible PC/MS-DOS
; SOFTWARE: WordPerfect version 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/714,960B
; FILING DATE: 17-SEP-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU RJ9065
; FILING DATE: 12-MAR-1990
; APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU91/00086
; FILING DATE: 12-MAR-1991
; APPLICATION NUMBER: US 07/930,415
; FILING DATE: 09-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/107,235
; FILING DATE: 16-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Resis, Robert H.
; REGISTRATION NUMBER: 32,168
; REFERENCE/DOCKET NUMBER: 92,622-B
; TELEPHONE: (312) 715-1000
; TELEFAX: (312) 715-1234
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 5..6
; OTHER INFORMATION: /product= "OTHER"
; /note= "CYS 5 (ACM) PROTECTION PERMANENT"
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..15
; OTHER INFORMATION: /note= "PEPTIDE 462"
US-08-714-960B-19

Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KGQGCPSSTHV 16
Db 1 KGQGCPSSTHV 10

RESULT 4
US-08-107-235-10
; Sequence 10, Application US/08107235
; Patent No. 5587457
; GENERAL INFORMATION:
; APPLICANT: Rathjen, Deborah A
; APPLICANT: Ferrante, Antonio
; APPLICANT: Widmer, Fred
; TITLE OF INVENTION: Neutrophil Stimulating Peptides
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff, Ltd.
; STREET: 10 S. Wacker Dr.
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/107,235
; FILING DATE: 16-AUG-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,415
; FILING DATE: 12-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McDonnell, John J
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 52,622A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..15
; OTHER INFORMATION: /note= "PEPTIDE 308 (54-68)"
US-08-107-235-10

Query Match 58.4%; Score 52; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSQVLFKQG 10
Db 6 YSQVLFKQG 15

RESULT 5
US-08-178-268-44
; Sequence 44, Application US/08178268
; Patent No. 5795859
; GENERAL INFORMATION:
; APPLICANT: RATHGEN, Deborah A
; APPLICANT: WIDMER, Fred
; APPLICANT: GRIGG, Geoffrey W

; APPLICANT: MACK, Phillip O
; TITLE OF INVENTION: Peptide which Abrogates TNF and/or LPS Toxicity
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon & Vanderhye P.C.
; STREET: 1100 No. 5795859th Giebe Road, 8th Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/178,268
; FILING DATE: 05-JAN-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: MITCHARD, Leonard C
; REGISTRATION NUMBER: 29,009
; REFERENCE/DOCKET NUMBER: 47-45
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: both
; MOLECULE TYPE: peptide
US-08-178-268-44

Query Match 58.4%; Score 52; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSQVLFKQG 10
Db 6 YSQVLFKQG 15

RESULT 6
US-08-714-960B-10
; Sequence 10, Application US/08714960B
; Patent No. 6121237
; GENERAL INFORMATION:
; APPLICANT: RATHJEN, Deborah A
; APPLICANT: FERRANTE, Antonio
; TITLE OF INVENTION: Neutrophil Stimulating Peptides
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER & WITCOFF, LTD.
; STREET: 10 S. Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 Mb storage diskette, 3.50 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: IBM compatible PC/MS-DOS
; SOFTWARE: WordPerfect version 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/714,960B
; FILING DATE: 17-SEP-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PJ9065
; FILING DATE: 12-MAR-1990
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/AU91/00086
FILING DATE: 12-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/930,415
FILING DATE: 09-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/107,235
FILING DATE: 16-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Resis, Robert H.
REGISTRATION NUMBER: 32,168
REFERENCE/DOCKET NUMBER: 92,622-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 715-1234
TELEFAX: (312) 715-1234
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
NAME/KEY: Peptide
LOCATION: 1..15
OTHER INFORMATION: /note= "PEPTIDE 308 (54-68)"
US-08-714-960B-10

Query Match 58.4%; Score 52; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSQVLFGKGG 10
DB 6 YSQVLFGKGG 15

RESULT 7
US-09-598-784-10
Sequence 10, Application US/09598784
Patent No. 6375928
GENERAL INFORMATION:
APPLICANT: RATHJEN, Deborah A
FERRANTE, Antonio
TITLE OF INVENTION: Neutrophil Stimulating Peptides
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER & WITCOFF, LTD.
STREET: 10 S. Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb storage diskette, 3.50 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: IBM compatible PC/MS-DOS
SOFTWARE: WordPerfect version 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/598,784
FILING DATE: 21-Jun-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU RJ9065
FILING DATE: 12-MAR-1990
APPLICATION NUMBER: PCT/AU91/00086
FILING DATE: 12-MAR-1991
APPLICATION NUMBER: US 07/930,415
FILING DATE: 09-NOV-1992
APPLICATION NUMBER: US 08/107,235
FILING DATE: 16-AUG-1993
APPLICATION NUMBER: US 08/714,960
FILING DATE: 17-SEP-1996

ATTORNEY/AGENT INFORMATION:
NAME: Resis, Robert H.
REGISTRATION NUMBER: 32,168
REFERENCE/DOCKET NUMBER: 11341.00001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 715-1000
TELEFAX: (312) 715-1234
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..15
OTHER INFORMATION: /note= "PEPTIDE 308 (54-68)"
US-09-598-784-10

Query Match 58.4%; Score 52; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSQVLFGKGG 10
DB 6 YSQVLFGKGG 15

RESULT 8
US-09-157-864-7
Sequence 7, Application US/09157864
Patent No. 6440694
GENERAL INFORMATION:
APPLICANT: Bienkowski, Michael J
APPLICANT: Mills, Cynthia J
APPLICANT: Jones, David A
TITLE OF INVENTION: TNF-Related Death Ligand
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pharmacia & Upjohn, Intellectual Property
ADDRESSEE: Legal Services
STREET: 301 Henrietta Street
CITY: Kalamazoo
STATE: MI
COUNTRY: USA
ZIP: 49001
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/157,864
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Kerber, Lori L.
REGISTRATION NUMBER: 41,113
REFERENCE/DOCKET NUMBER: 6111.N CN1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 616/833-0974
TELEFAX: 616/833-8897
TELEX: 224401
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-157-864-7

Query Match 39.3%; Score 35; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSQVLFK 7
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Db 10 YSQVLFK 16

RESULT 9
US-08-406-330-43
; Sequence 43, Application US/08406330
; Patent No. 5817748
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MINOTOPE AND ANTI-MINOTOPE OF
; TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN Ib/IX
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406,330
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Timian, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 20884/100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-406-330-43

Query Match 34.8%; Score 31; DB 2; Length 12;
Best Local Similarity 62.5%; Pred. No. 41;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 5 LFKGOGCP 12
||:| ||
Db 5 LFRGPRCP 12

RESULT 10
US-08-556-597-43
; Sequence 43, Application US/08556597
; Patent No. 587155
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MINOTOPE AND ANTI-MINOTOPE OF
; TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN Ib/IX
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP

; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/556,597
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,330
; FILING DATE: 17-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Timian, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 20884/101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-556-597-43

Query Match 34.8%; Score 31; DB 2; Length 12;
Best Local Similarity 62.5%; Pred. No. 41;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 5 LFKGOGCP 12
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Db 5 LFRGPRCP 12

RESULT 11
US-09-518-046-143
; Sequence 143, Application US/09518046
; Patent No. 6294663
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: Transmembrane Serine Protease Overexpressed
; TITLE OF INVENTION: in Ovarian Carcinoma and Uses Thereof
; FILE REFERENCE: D6192CIP
; CURRENT APPLICATION NUMBER: US/09/518,046
; CURRENT FILING DATE: 2000-03-02
; EARLIER APPLICATION NUMBER: 09/261,416
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 143
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; LOCATION: 192...200
; OTHER INFORMATION: TADG-12 peptide
US-09-518-046-143

Query Match 33.7%; Score 30; DB 4; Length 9;
Best Local Similarity 62.5%; Pred. No. 2e+05;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 9 QGCPSTHV 16
:||| ||
Db 2 EGCASGHV 9

RESULT 12
US-08-253-678A-19
; Sequence 19, Application US/08253678A
; Patent No. 5997844
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T.
; APPLICANT: Buttram, Scott
; APPLICANT: McBride, William
; APPLICANT: Lister-James, John
; APPLICANT: Civitello, Edgar R.
; TITLE OF INVENTION: TECHNETIUM-99m LABELED PEPTIDES FOR
; TITLE OF INVENTION: IMAGING
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Diatide, Inc.
; STREET: 9 Delta Drive
; CITY: Londonderry
; STATE: NH
; COUNTRY: USA
; ZIP: 03053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/253,678A
; FILING DATE: 03-JUN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: McDaniels, Patricia A.
; REGISTRATION NUMBER: 33,194
; REFERENCE/DOCKET NUMBER: DITI 112
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (603) 437-8970
; TELEFAX: (603) 437-8977
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /product= "methionine 1 is
; OTHER INFORMATION: formylated"
; OTHER INFORMATION: /label= formyl
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /product= "lysine 4 is linked to a
; OTHER INFORMATION: BAT chelator"
; OTHER INFORMATION: /label= BAT
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 10
; OTHER INFORMATION: /product= "serine 10 is amidated"
; OTHER INFORMATION: /label= amide
US-08-253-678A-19

Query Match 32.6%; Score 29; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 73;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 4 VLFKGGCGPS 13
Db 1 MLFKGSGSGS 10

RESULT 13
US-08-582-134B-19
; Sequence 19, Application US/08582134B
; Patent No. 6074627
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T.
; APPLICANT: Buttram, Scott
; APPLICANT: McBride, William
; APPLICANT: Lister-James, John
; APPLICANT: Civitello, Edgar R.
; TITLE OF INVENTION: TECHNETIUM-99m LABELED PEPTIDES FOR
; TITLE OF INVENTION: IMAGING
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Diatide, Inc.
; STREET: 9 Delta Drive
; CITY: Londonderry
; STATE: NH
; COUNTRY: USA
; ZIP: 03053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/582,134B
; FILING DATE: 14-MAY-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: McDaniels, Patricia A.
; REGISTRATION NUMBER: 33,194
; REFERENCE/DOCKET NUMBER: DITI 112D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (603) 437-8970
; TELEFAX: (603) 437-8977
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /product= "methionine 1 is
; OTHER INFORMATION: formylated"
; OTHER INFORMATION: /label= formyl
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /product= "lysine 4 is linked to a
; OTHER INFORMATION: BAT chelator"
; OTHER INFORMATION: /label= BAT
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 10
; OTHER INFORMATION: /product= "serine 10 is amidated"
; OTHER INFORMATION: /label= amide
US-08-582-134B-19

Query Match 32.6%; Score 29; DB 3; Length 10;
Best Local Similarity 60.0%; Pred. No. 73;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 4 VLFKGGCGPS 13
Db 1 MLFKGSGSGS 10

RESULT 14
US-08-598-873-54

; Sequence 54, Application US/08598873
; Patent No. 5928884
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo M.
; APPLICANT: Huebner, Kay
; TITLE OF INVENTION: PHIT PROTEINS AND NUCLEIC ACIDS AND
; TITLE OF INVENTION: METHODS BASED THEREON
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/598,873
; FILING DATE: 09-FEB-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Friebel, Thomas E.
; REGISTRATION NUMBER: 29,258
; REFERENCE/DOCKET NUMBER: 8666-004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-598-873-54

Query Match 32.6%; Score 29; DB 2; Length 11;
Best Local Similarity 62.5%; Pred. No. 81;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 FKGGGCPs 13
| | | | |
Db 2 FSKQNCPS 9

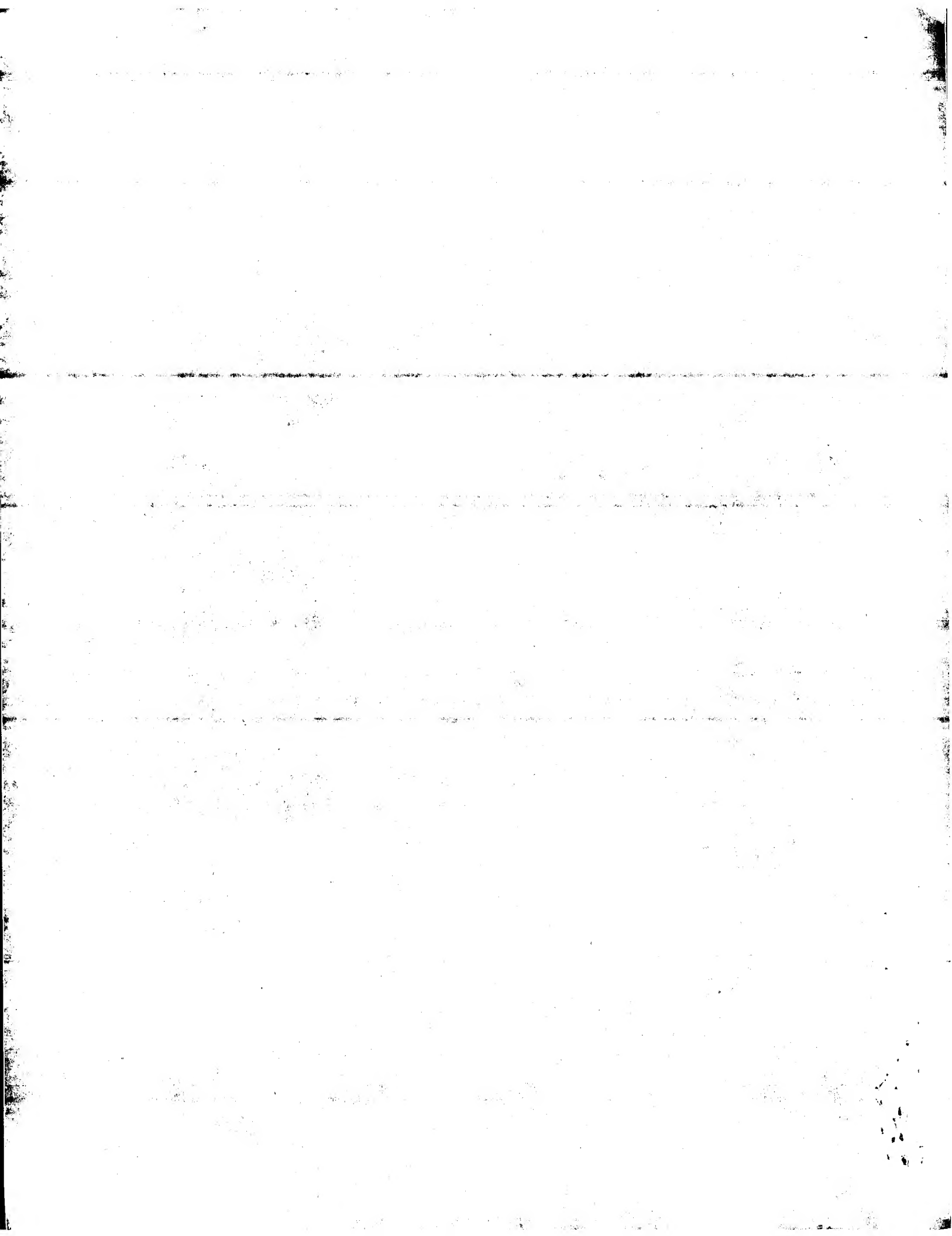
RESULT 15
US-08-605-430-54
; Sequence 54, Application US/08605430
; Patent No. 6242212
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo M.
; APPLICANT: Huebner, Kay
; TITLE OF INVENTION: PHIT PROTEINS AND NUCLEIC ACIDS AND
; TITLE OF INVENTION: METHODS BASED THEREON
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/605,430

; FILING DATE: 22-FEB-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Friebel, Thomas E.
; REGISTRATION NUMBER: 29,258
; REFERENCE/DOCKET NUMBER: 8666-005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-605-430-54

Query Match 32.6%; Score 29; DB 4; Length 11;
Best Local Similarity 62.5%; Pred. No. 81;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 FKGGGCPs 13
| | | | |
Db 2 FSKQNCPS 9

Search completed: December 4, 2002, 13:32:51
Job time : 15 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 4, 2002, 13:35:35 ; Search time 15 seconds
(without alignments)
140.997 Million cell updates/sec

Title: US-09-754-004-2

Perfect score: 115

Sequence: 1 YQTKVNLSSAIKSPCQRETPG 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 4263

Minimum DB seq length: 0

Maximum DB seq length: 22

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	27.0	18	2	A60118
2	27	23.5	20	2	S31220
3	26	22.6	15	2	A41338
4	26	22.6	18	2	S46418
5	26	22.6	18	2	I59649
6	26	22.6	20	2	I53671
7	26	22.6	20	2	B56894
8	25	21.7	22	2	A33816
9	24	20.9	15	2	PT0092
10	24	20.9	18	2	B24867
11	23	20.0	9	2	PH1591
12	23	20.0	13	2	A32453
13	23	20.0	16	2	A54877
14	23	20.0	16	2	PH0767
15	23	20.0	19	2	PC1315
16	23	20.0	22	2	B81078
17	22	19.1	14	2	I56493
18	22	19.1	15	2	PA0024
19	22	19.1	16	2	B54877
20	22	19.1	17	2	PC2196
21	22	19.1	19	2	E56661
22	22	19.1	20	2	A33878
23	22	19.1	20	2	D37396
24	22	19.1	21	2	D22565
25	22	19.1	21	2	H71858
26	22	19.1	21	2	I54268
27	22	19.1	21	2	S47207
28	21	18.3	10	2	S62880
29	21	18.3	13	2	PQ0491

30 21 18.3 13 2 D56661 S-locus specific g
31 21 18.3 14 2 I56388 Km(r) protein - Es
32 21 18.3 15 2 B56661 S-locus specific g
33 21 18.3 15 2 S36896 ribosomal protein
34 21 18.3 16 2 PH1589 Ig H chain V-D-J r
35 21 18.3 16 2 PH0763 T-cell receptor be
36 21 18.3 18 2 S29491 GTP-binding protei
37 21 18.3 19 2 S38895 kmR protein - yeas
38 21 18.3 19 2 JP0063 ribosomal protein
39 21 18.3 19 2 C56661 S-locus specific g
40 21 18.3 19 2 PQ0492 self-incompatibili
41 21 18.3 20 2 S37684 protein IEF SSP 91
42 21 18.3 20 2 B47642 T-cell surface gly
43 21 18.3 21 2 S68914 ribosomal protein
44 21 18.3 22 2 G83924 hypothetical prote
45 20 17.4 10 2 C26997 unspecific monoxy

ALIGNMENTS

RESULT 1

A60118

22K protein - Lyme disease spirochete (fragment)

C:Species: Borrelia burgdorferi (Lyme disease spirochete)

C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 18-Jun-1993

C:Accession: A60118

R:Luft, B.J.; Jiang, W.; Munoz, P.; Dattwyler, R.J.; Gorevic, P.D.

Infect. Immun. 57, 3637-3645, 1989

A:Title: Biochemical and immunological characterization of the surface proteins of Bo

A:Reference number: A60118; MUID:90035442; PMID:2807540

A:Accession: A60118

A:Molecule type: protein

A:Residues: 1-18 <LUF>

Query Match 27.0%; Score 31; DB 2; Length 18;

Best Local Similarity 66.7%; Pred. No. 1.4e+02;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 KVNLLSAIK 12

Db 9 KINLLXAIQ 17

RESULT 2

S31220

82K protein - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 17-Mar-1999

C:Accession: S31220

R:Castillo, G.M.; Templeton, D.M.

FEBS Lett. 318, 292-296, 1993

A:Title: Subunit structure of bovine ESF (extracellular-matrix stabilizing factor(s))

A:Reference number: S31219; MUID:93178646; PMID:7680011

A:Accession: S31220

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-20 <CAS>

Query Match 23.5%; Score 27; DB 2; Length 20;

Best Local Similarity 83.3%; Pred. No. 7e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YQTKVN 6

Db 13 YSTKVN 18

RESULT 3

A41338

isocitrate lyase (EC 4.1.3.1) - Acinetobacter calcoaceticus (fragment)

C:Species: Acinetobacter calcoaceticus

C:Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 23-Jun-1993

```
C;Accession: A41338
R;Hoyt, J.C.; Johnson, K.E.; Reeves, H.C.
J. Bacteriol. 173, 6844-6848, 1991
A;Title: Purification and characterization of Acinetobacter calcoaceticus isocitrate lyase
A;Reference number: A41338; MUID:92041568; PMID:1938889
A;Accession: A41338
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <HO>
C;Keywords: carbon-carbon lyase; oxo-acid-lyase

Query Match      22.6%; Score 26; DB 2; Length 15;
Best Local Similarity 30.8%; Pred. No. 7.5e+02;
Matches 4; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 YQTKVNLLSAIKS 13
    ||| : : : : :
Db 3 YQTAIDAVRELKA 15

RESULT 4
S46418
NTLL protein - curled-leaved tobacco
C;Species: Nicotiana plumbaginifolia (curled-leaved tobacco)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 02-Aug-2002
C;Accession: S46418
R;Daniel-Vedele, F.; Caboche, M.
Mol. Gen. Genet. 240, 365-373, 1993
A;Title: A tobacco cDNA clone encoding a GATA-1 zinc finger protein homologous to regula
A;Reference number: S46418; MUID:94019241; PMID:8413186
A;Accession: S46418
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-18 <DAN>
A;Cross-references: EMBL:S65745
C;Superfamily: Arabidopsis thaliana GATA transcription factor 4

Query Match      22.6%; Score 26; DB 2; Length 18;
Best Local Similarity 54.5%; Pred. No. 9.1e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 12 KSPCORETPG 22
    ||| ||| |
Db 4 KTPQWREGPLG 14

RESULT 5
I59649
human leukocyte antigen alpha chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C;Accession: I59649
R;Fogdell, A.; Olerup, O.
Tissue Antigens 44, 19-24, 1994
A;Title: The DOA1*0104 allele is carried by DRB1*1401-positive haplotypes
A;Reference number: I59649; MUID:95064785; PMID:7974465
A;Accession: I59649
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-18 <RES>
A;Cross-references: GB:S75685; NID:g913771; PIDN:AAB32621.1; PID:g913772
C;Genetics:
A;Gene: GDB:HLA-DQA1
A;Cross-references: GDB:120638; OMIM:146880
A;Map position: 6p21.3-6p21.3

Query Match      22.6%; Score 26; DB 2; Length 18;
Best Local Similarity 45.5%; Pred. No. 9.1e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 8 LSAIKSPCORE 18
    | : ||| |
Db 5 LSAIKSPCORE 15

RESULT 6
I53671
neurofilament heavy subunit - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C;Accession: I53671
R;Figlewicz, D.A.; Rouleau, G.A.; Krizus, A.; Julien, J.P.
Gene 132, 297-300, 1993
A;Title: Polymorphism in the multi-phosphorylation domain of the human neurofilament
A;Reference number: I53671; MUID:94040777; PMID:8224877
A;Accession: I53671
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-20 <RES>
A;Cross-references: GB:S66488; NID:g452861; PIDN:AAB28609.1; PID:g452862
C;Genetics:
A;Gene: GDB:NEFH
A;Cross-references: GDB:120225; OMIM:162230
A;Map position: 22q12.1-22q13.1

Query Match      22.6%; Score 26; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 1e+03;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 12 KSPCORETPE 21
    ||| : : : ||
Db 6 KSPEKAKSPE 15

RESULT 7
B56894
intracytostalline chromoprotein 1 - Waltonia inconspicua (fragment)
C;Species: Waltonia inconspicua
C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 20-Jun-2000
C;Accession: B56894
R;Cusack, M.; Curry, G.; Clegg, H.; Abbott, G.
Comp. Biochem. Physiol. B 102, 93-95, 1992
A;Title: An intracytostalline chromoprotein from red brachiopod shells: implications f
A;Reference number: A56894; MUID:92405551; PMID:1526140
A;Contents: Sowerby, red brachiopod shells
A;Accession: B56894
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-20 <CUS>
A;Note: sequence extracted from NCBI backbone (NCBIP:114883)
C;Keywords: chromoprotein

Query Match      22.6%; Score 26; DB 2; Length 20;
Best Local Similarity 35.7%; Pred. No. 1e+03;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 YQTKVNLLSAIKSP 14
    | | : : | : |
Db 7 YATMISKTSQAKNP 20

RESULT 8
A33816
Ca2+-transporting ATPase (EC 3.6.3.8) - human (fragments)
C;Species: Homo sapiens (man)
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 19-Apr-2002
C;Accession: A33816
R;James, P.; Vorherr, T.; Krebs, J.; Morelli, A.; Castello, G.; McCormick, D.J.; Penn
J. Biol. Chem. 264, 8289-8296, 1989
A;Title: Modulation of erythrocyte Ca(2+)-ATPase by selective calpain cleavage of the
A;Reference number: A33816; MUID:89255268; PMID:2542272
A;Accession: A33816
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-22 <JAM>
C;Keywords: hydrolase
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Query Match 21.7% Score 25; DB 2; Length 22;
Best Local Similarity 33.3% Pred. No. 1.7e+03;
Matches 4; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 QTKVNLISAKS 13
| | | : : : | |
DB 3 QTIKVVNAFSS 14

RESULT 9

PT0092

NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) 24k chain - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 03-Jun-2002

C:Accession: PT0092

R:Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Morinasa, T.; Tsugita, A.

submitted to JIPID, July 1998

A:Description: Proteome analysis of mouse brain.

A:Reference number: PT0091

A:Accession: PT0092

A:Molecule type: protein

A:Residues: 1-15 <KAW>

A:Experimental source: brain, striatum

C:Keywords: NAD; oxidoreductase

Query Match 20.9% Score 24; DB 2; Length 15;
Best Local Similarity 80.0% Pred. No. 1.6e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 17 RETPE 21
| | | | |
DB 10 RDTPE 14

RESULT 10

B24867

scylorhinin II - smaller spotted catshark

C:Species: Scyliorhinus canicula (smaller spotted catshark, smaller spotted dogfish)

C:Date: 02-Jun-1988 #sequence_revision 02-Jun-1988 #text_change 08-Dec-1995

C:Accession: B24867

R:Conlon, J.M.; Deacon, C.F.; O'Toole, L.; Thim, L.

FEBS Lett. 200, 111-116, 1986

A:Title: Scylorhinin I and II: two novel tachykinins from dogfish gut.

A:Reference number: A91359; MUID:86192829; PMID:2422058

A:Accession: B24867

A:Molecule type: protein

A:Residues: 1-18 <CON>

C:Keywords: amidated carboxyl end; neuropeptide

F:18/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 20.9% Score 24; DB 2; Length 18;
Best Local Similarity 40.0% Pred. No. 1.9e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 13 SPCQRETPG 22
| | : | | |
DB 1 SPSNSKCPDG 10

RESULT 11

PH1591

Ig H chain V-D-J region (wild-type clone 142) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999

C:Accession: PH1591

R:Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice

A:Reference number: PH1580; MUID:93301609; PMID:8315387

A:Accession: PH1591

A:Molecule type: DNA

A:Residues: 1-9 <LEV>

A:Experimental source: bone marrow pre-B lymphocyte
C:Keywords: Immunoglobulin

Query Match 20.0% Score 23; DB 2; Length 9;
Best Local Similarity 50.0% Pred. No. 2.8e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 15 CQRETPG 22
| | : | | |
DB 1 CARGSPYG 8

RESULT 12

A32453

phloroglucinol reductase (EC 1.-.-.-) - Eubacterium oxidoreducens (fragment)

C:Species: Eubacterium oxidoreducens

C:Date: 26-Oct-1989 #sequence_revision 26-Oct-1989 #text_change 24-Oct-1998

C:Accession: A32453

R:Haddock, J.D.; Ferry, J.G.

J. Biol. Chem. 264, 4423-4427, 1989

A:Title: Purification and properties of phloroglucinol reductase from Eubacterium oxi

A:Reference number: A32453; MUID:89174692; PMID:2925649

A:Accession: A32453

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-13 <HAD>

C:Keywords: oxidoreductase

Query Match 20.0% Score 23; DB 2; Length 13;
Best Local Similarity 60.0% Pred. No. 2e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 14 PCQRE 18
| | : |
DB 3 PCNKE 7

RESULT 13

A54877

alpha-conotoxin PnIA [validated] - cone shell (Conus pennaceus)

N:Alternate names: alpha-Ctx-PnIA

C:Species: Conus pennaceus

C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 15-Sep-2000

C:Accession: A54877

R:Fainzilber, M.; Hasson, A.; Oren, R.; Burlingame, A.L.; Gordon, D.; Spira, M.E.; Zl

Biochemistry 33, 9523-9529, 1994

A:Title: New mollusc-specific alpha-conotoxins block Aplysia neuronal acetylcholine r

A:Reference number: A54877; MUID:94347719; PMID:8068627

A:Accession: A54877

A:Molecule type: protein

A:Residues: 1-16 <FAI>

R:Hu, S.H.; Gehrman, J.; Guddat, L.W.; Alewood, P.F.; Craik, D.J.; Martin, J.L.

submitted to the Brookhaven Protein Data Bank, January 1996

A:Reference number: A66355; PDB:1PEN

A:Contents: annotation; X-ray crystallography, 1.1 angstroms; residues 1-16

C:Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsyn

C:Superfamily: alpha-conotoxin

C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neu

F:2-8,3-16/Disulfide bonds: #status experimental

F:16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 20.0% Score 23; DB 2; Length 16;
Best Local Similarity 37.5% Pred. No. 2.5e+03;
Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 14 PCQRETPG 21
| | : | |
DB 7 PCAANNPD 14

RESULT 14

PH0767

T-cell receptor beta chain (J5) - mouse (fragment)

C:Species: Mus musculus (house mouse)
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
 C:Accession: PH0767
 R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
 J. Exp. Med. 174, 1371-1383, 1991
 A:Title: T cell receptor genes in a series of class I major histocompatibility complex-I allelic exclusion and antigen-specific repertoire.
 A:Reference number: PH0746; MUID:92078846; PMID:1836010
 A:Accession: PH0767
 A:Molecule type: mRNA
 A:Residues: 1-16 <CAS>
 A:Cross-references: EMBL:X60861; NID:g52752; PIDN:CAA43251.1; PID:g52753
 A:Experimental source: T lymphocyte
 C:Keywords: T-cell receptor

Query Match 20.0%; Score 23; DB 2; Length 16;
 Best Local Similarity 37.5%; Pred. No. 2.5e+03;
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 15 CORETPEG 22
 | :|:
 Db 1 CASSSPQG 8

RESULT 15

PC1315

large granule L2 chain - horseshoe crab (Tachyplesus tridentatus) (fragment)
 C:Species: Tachyplesus tridentatus

C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999
 C:Accession: PC1315

R:Shigenaga, T.; Takayenoki, Y.; Kawasaki, S.; Seki, N.; Muta, T.; Toh, Y.; Ito, A.; Iwa
 J. Biochem. 114, 307-316, 1993

A:Title: Separation of large and small granules from horseshoe crab (Tachyplesus tridenta
 A:Reference number: PC1309; MUID:94110249; PMID:8282718

A:Accession: PC1315

A:Molecule type: protein

A:Residues: 1-19 <SHI>

C:Comment: This protein participates in immobilization of invading microbes.

Query Match 20.0%; Score 23; DB 2; Length 19;
 Best Local Similarity 66.7%; Pred. No. 3e+03;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QTKVNL 7
 |||:
 Db 8 QTKLNV 13

Search completed: December 4, 2002, 13:37:45
 Job time : 16 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 4, 2002, 13:32:55 ; Search time 11 seconds

(without alignments)

82.953 Million cell updates/sec

Title: US-09-754-004-2

Perfect score: 115

Sequence: 1 YQTKVNLSSAIKSPCQRETPG 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 1277

Minimum DB seq length: 0

Maximum DB seq length: 22

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	26	22.6	15	1	ACEA_ACICA
2	24	20.9	18	1	TKN2_SCYCA
3	23	20.0	13	1	PHGR_EUROX
4	23	20.0	16	1	CXAA_CONPE
5	23	20.0	19	1	TRP3_LEUMA
6	22	19.1	15	1	FKB7_PINPS
7	22	19.1	16	1	CXAB_CONPE
8	21	18.3	8	1	UH09_RAT
9	21	18.3	13	1	UN41_CLOPA
10	21	18.3	20	1	CD4_SHEEP
11	21	18.3	20	1	JHBP_BOMMO
12	20	17.4	10	1	COXM_RAT
13	20	17.4	15	1	ARCA_STRP5
14	20	17.4	15	1	CXAA_CONAL
15	20	17.4	16	1	OTPB_SOLTU
16	20	17.4	16	1	ADPB_CERSI
17	20	17.4	17	1	CXMA_CONPE
18	20	17.4	17	1	CXMB_CONPE
19	20	17.4	17	1	UP41_UPEIN
20	20	17.4	21	1	GLGI_SPIOL
21	20	17.4	22	1	LPL_CORGL
22	19	16.5	9	1	MGMT_BOVIN
23	19	16.5	13	1	RS19_ASHYP
24	19	16.5	14	1	SODN_STRGR
25	19	16.5	16	1	HBD_CLOPA
26	19	16.5	17	1	GSXK_PINPS
27	19	16.5	18	1	FXRX_RHILE
28	19	16.5	19	1	LCRP_PETMA
29	19	16.5	19	1	OXLA_OPHHA
30	19	16.5	20	1	CATA_ACIRA
31	19	16.5	20	1	OMPI_ACITAC
32	19	16.5	21	1	SCIB_BPT5
33	19	16.5	21	1	THAN_PODMA

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RESULT 1
ACEA_ACICA
ID ACEA_ACICA STANDARD; PRT; 15 AA.
AC P28467;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Isocitrate lyase (EC 4.1.3.1) (Isocitrate) (Isocitratase) (ICL)
DE (Fragment).
GN ACEA
OS Acinetobacter calcoaceticus.
OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
OC Acinetobacter.
OX NCBI_TaxID=471;
RN [1]
RP SEQUENCE
RX MEDLINE=92041568; PubMed=1938889;
RA Hoyt J.C., Johnson K.E., Reeves H.C.;
RT "Purification and characterization of Acinetobacter calcoaceticus
RT isocitrate lyase."
RL J. Bacteriol. 173:6844-6848(1991).
CC -|- CATALYTIC ACTIVITY: Isocitrate -> succinate + glyoxylate.
CC -|- PATHWAY: FIRST STEP IN GLYOXYLATE BYPASS, AN ALTERNATIVE TO THE
CC TRICARBOXYLIC ACID CYCLE (IN BACTERIA, PLANTS, AND FUNGI).
CC -|- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -|- SUBCELLULAR LOCATION: Cytoplasmic.
CC -|- SIMILARITY: BELONGS TO THE ISOCITRATE LYASE FAMILY.
DR PIR: A41338; A41338.
DR InterPro: IPR00918; Isocit_lyase.
DR PROSITE; PS00161; ISOCITRATE_LYASE; PARTIAL.
KW Glyoxylate bypass; Tricarboxylic acid cycle; Lyase.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1710 MW; 83AE726B1F2F96E3 CRC64;

Query Match 22.6%; Score 26; DB 1; Length 15;
Best Local Similarity 30.8%; Pred. No. 3.5e+02;
Matches 4; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy . 1 YQTKVNLSSAIK 13
||| : : : :
Db 3 YQTAIDAVRELKA 15

RESULT 2
TKN2_SCYCA STANDARD; PRT; 18 AA.
AC P08609;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Scyllorhinin II (Rectin).
OS Scyllorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyllorhinidae; Scyllorhinus.
OX NCBI_TaxID=7830;
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Q64133 mus musculu
P05486 conus geogr
P80975 thunnus obe
P24047 stomopneute
P80466 comamonas t
P08951 rana pipien
P56920 rana tempor
P12801 anas platyr
P80607 zea mays (m
P23436 rattus norv
P80605 rhizobium 1

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RN SEQUENCE.
RP MEDLINE=86192829; PubMed=2422058;
RA Conlon J.M., Deacon C.F., O'Toole L., Thim L.;
RT "Scyllorhinin I and II: two novel tachykinins from dogfish gut.";
RL FEBS Lett. 200;111-116(1986).
RN SEQUENCE.
RP TISSUE=Small intestine;
RX MEDLINE=95335921; PubMed=7541963;
RA Anderson W.G., Conlon J.M., Hazon N.;
RT "Characterization of the endogenous intestinal peptide that
stimulates the rectal gland of Scyllorhinus canicula.";
RL Am. J. Physiol. 268:R1359-R1364(1995).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
MUSCLES.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; B24867; B24867.
DR InterPro: IPR002040; Tachykinin.
DR Pfam: PF02202; Tachykinin; 1.
DR PROSITE: PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation.
FT DISULFID 7 13
FT MOD_RES 18 18
SQ SEQUENCE 18 AA; 1854 MW; FCCA3FB01E2F3907 CRC64;

Query Match 20.9%; Score 24; DB 1; Length 18;
Best Local Similarity 40.0%; Pred. No. 9e+02; Indels 0; Gaps 0;
Matches 4; Conservative 2; Mismatches 4;

QY 13 SPCQRETPG 22
DB 1 SPSNSKCPDG 10

RESULT 3
PHGR_EUBOX
ID PHGR_EUBOX STANDARD; PRT; 13 AA.
AC P57793;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Phloroglucinol reductase (EC 1.3.1.57) (Fragment).
OS Eubacterium oxidoreducens
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Eubacteriaceae;
OC Eubacterium.
OX NCBI_TaxID=1732;
RN SEQUENCE, AND CHARACTERIZATION.
RP STRAIN=G-41;
RX MEDLINE=89174692; PubMed=2925649;
RA Haddock J.D., Ferry J.G.;
RT "Purification and properties of phloroglucinol reductase from
Eubacterium oxidoreducens G-41.";
RL J. Biol. Chem. 264:4423-4427(1989).
CC -!- FUNCTION: FUNCTIONS IN THE PATHWAY OF ANAEROBIC DEGRADATION OF
TRIHYDROXYBENZENES BY CATALYZING REDUCTION OF THE AROMATIC NUCLEUS
PRIOR TO RING FISSION.
CC -!- CATALYTIC ACTIVITY: Dihydrophloroglucinol + NADP(+) =
phloroglucinol + NADPH.
CC -!- SUBUNIT: HOMODIMER.
CC -!- MISCELLANEOUS: TEMPERATURE AND PH OPTIMA ARE 40 DEGREES CELSIUS
AND 7.8 IN THE FORWARD DIRECTION.
KW Aromatic hydrocarbons catabolism; Oxidoreductase; NADP.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1527 MW; 427E2E0833F1CB13 CRC64;

Query Match 20.0%; Score 23; DB 1; Length 13;
Best Local Similarity 60.0%; Pred. No. 9.3e+02; Indels 0; Gaps 0;
Matches 3; Conservative 1; Mismatches 1;


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QY 14 PCQRE 18
DB 3 PCNKE 7

RESULT 4
CXAA_CONPE STANDARD; PRT; 16 AA.
ID CXAA_CONPE
AC P50984;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Alpha-conotoxin PnIA.
OS Conus pennaceus (Feathered cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=37335;
RN SEQUENCE.
RP TISSUE=Venom;
RX MEDLINE=94347719; PubMed=8068627;
RA Fainzilber M., Hasson A., Oren R., Burlingame A.L., Gordon D.,
RA Spira M.E., Zlotkin E.;
RT "New mollusc-specific alpha-conotoxins block Aplysia neuronal
acetylcholine receptors.";
RL Biochemistry 33:9523-9529(1994).
RN Sulfation of Tyr-15.
RP MEDLINE=99242956; PubMed=10226369;
RA Wolfender J.B., Chu F., Ball H., Wolfender F., Fainzilber M.,
RA Baldwin M.A., Burlingame A.L.;
RT "Identification of tyrosine sulfation in Conus pennaceus conotoxins
alpha-PnIA and alpha-PnIB: further investigation of labile sulfo- and
phosphopeptides by electrospray, matrix-assisted laser
desorption/ionization (MALDI) and atmospheric pressure MALDI mass
spectrometry.";
RL J. Mass Spectrom. 34:447-454(1999).
RN X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).
RP MEDLINE=96311277; PubMed=8740364;
RA Hu S.-H., Gehrmann J., Guddat L.W., Alewood P.F., Craik D.J.,
RA Martin J.L.;
RT "The 1.1 A crystal structure of the neuronal acetylcholine receptor
antagonist, alpha-conotoxin PnIA from Conus pennaceus.";
RL Structure 4:417-423(1996).
CC -!- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES. THEY
BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR), AND THUS
INHIBIT THEM. IN CONTRAST TO OTHER ALPHA-CONOTOXINS, WHICH ARE
SELECTIVE FOR VERTEBRATE SKELETAL MUSCLE NACHR, THE CONUS
PENNACEUS ALPHA-CONOTOXINS BLOCK NACHR IN MOLLUSKS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
FAMILY.
DR PDB; IPEN; 2I-APR-97.
KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
KW Acetylcholine receptor inhibitor; Amidation; Sulfation; 3D-structure.
FT DISULFID 2 8
FT DISULFID 3 16
FT MOD_RES 15 15
FT MOD_RES 16 16
SQ SEQUENCE 16 AA; 1628 MW; 05310FF95EC99005 CRC64;

Query Match 20.0%; Score 23; DB 1; Length 16;
Best Local Similarity 37.5%; Pred. No. 1.1e+03; Indels 0; Gaps 0;
Matches 3; Conservative 1; Mismatches 4;

QY 14 PCQRETP 21
DB 7 PCAANNPD 14

RESULT 5

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TRP3_LEUMA
ID TRP3_LEUMA STANDARD; PRT; 19 AA.
AC P81735;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Tachykinin-related peptide 3 (LemTRP 3).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE.
RC TISSUE=Midgut;
RX MEDLINE=97053012; PubMed=8897641;
RA Muren J.E., Naessel D.R.;
RT "Isolation of five tachykinin-related peptides from the midgut of
RT the cockroach Leucophaea maderae: existence of N-terminally extended
RT isoforms.";
RL Regul. Pept. 65:185-196(1996).
CC -1- FUNCTION: MYOACTIVE PEPTIDE. INCREASES THE AMPLITUDE AND FREQUENCY
CC OF SPONTANEOUS CONTRACTIONS AND TONUS OF HINDGUT MUSCLE.
CC -1- TISSUE SPECIFICITY: MIDGUT.
CC Tachykinin; Neuropeptide; Amidation.
KW MOD_RES 19 19
FT MOD_RES 19 19
SQ SEQUENCE 19 AA; 1930 MW; 99B5471A011625E5 CRC64;

Query Match 20.0%; Score 23; DB 1; Length 19;
Best Local Similarity 27.3%; Pred. No. 1.4e+03;
Matches 3; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 12 KSPQRETPPEG 22
DB 4 RAPGSKKAPS 14

RESULT 6
FKB7_PINPS
ID FKB7_PINPS STANDARD; PRT; 15 AA.
AC P81104;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 70 kDa peptidylprolyl isomerase (EC 5.2.1.8) (Peptidylprolyl cis-trans
DE isomerase) (Cyclophilin) (PPIase) (Si205-06) (fragment).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]
RP SEQUENCE.
RC TISSUE=Needle;
RX Plomion C., Costa P., Bahrman N., Frigerio J.-M.;
RA "Genetic analysis of needle proteins in maritime pine. 1. Mapping
RT dominant and codominant protein markers assayed on diploid tissue, in
RT a haploid-based genetic map.";
RL Salvia Genetica 46:161-165(1997).
RN [2]
RP SEQUENCE.
RC TISSUE=Needle;
RX MEDLINE=99274088; PubMed=10344291;
RA Costa P., Plomion C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -1- FUNCTION: PPIASE THAT BINDS CALMODULIN (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:
CC 5.3, ITS MW IS: 72 kDa.

CC -1- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
DR InterPro: IPR001179; FKBP_PPIase.
DR PROSITE: PS00453; FKBP_PPIASE_1; PARTIAL.
DR PROSITE: PS00454; FKBP_PPIASE_2; PARTIAL.
DR PROSITE: PS00559; FKBP_PPIASE_3; PARTIAL.
KW Isomerase; Rotamase; Repeat; Calmodulin-binding.
FT NON_TER 1 15
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1675 MW; 2B53999722277F3F CRC64;

Query Match 19.1%; Score 22; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 ETPE 21
DB 6 ETPE 9

RESULT 7
CXAB_CONPE
ID CXAB_CONPE STANDARD; PRT; 16 AA.
AC P50985;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Alpha-conotoxin PnIB.
OS Conus pennaceus (Feathered cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=37335;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=94347719; PubMed=8068627;
RA Fainzilber M., Hasson A., Oren R., Burlingame A.L., Gordon D.,
RA Spira M.E., Zlotkin E.;
RT "New mollusc-specific alpha-conotoxins block Aplysia neuronal
RT acetylcholine receptors.";
RL Biochemistry 33:9523-9529(1994).
RN [2]
RP SULFATION OF TYR-15.
RX MEDLINE=99242956; PubMed=10226369;
RA Wolfender J.L., Chu F., Ball H., Wolfender F., Fainzilber M.,
RA Baldwin M.A., Burlingame A.L.;
RT "Identification of tyrosine sulfation in Conus pennaceus conotoxins
RT alpha-PnIA and alpha-PnIB: further investigation of labile sulfo- and
RT phosphopeptides by electrospray, matrix-assisted laser
RT desorption/ionization (MALDI) and atmospheric pressure MALDI mass
RT spectrometry.";
RL J. Mass Spectrom. 34:447-454(1999).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).
RX MEDLINE=97444322; PubMed=9298951;
RA Hu S.H., Gehrmann J., Alewood P.F., Craik D.J., Martin J.L.;
RT "Crystal structure at 1.1-A resolution of alpha-conotoxin PnIB:
RT comparison with alpha-conotoxins PnIA and GI.";
RL Biochemistry 36:11323-11330(1997).
CC -1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
CC INHIBIT THEM. IN CONTRAST TO OTHER ALPHA-CONOTOXINS, WHICH ARE
CC SELECTIVE FOR VERTEBRATE SKELETAL MUSCLE NACHR, THE CONUS
CC PENNACEUS ALPHA-CONOTOXINS BLOCK NACHR IN MOLLUSKS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
CC FAMILY.
DR PDB: IAKG: 20-MAY-98.
KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
KW Acetylcholine receptor inhibitor; Amidation; Sulfation; 3D-structure.
FT DISULFID 2 8
FT DISULFID 3 16
FT MOD_RES 15 15
SQ SEQUENCE 15 AA; 1675 MW; 2B53999722277F3F CRC64;

```
FT MOD_RES 16 16 AMIDATION.
SQ SEQUENCE 16 AA; 1643 MW; 05310FF95ED86AF5 CRC64;

Query Match 19.1%; Score 22; DB 1; Length 16;
Best Local Similarity 37.5%; Pred. No. 1.7e+03;
Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 14 PCQRETP 21
II I:
Db 7 PCALSNPD 14
STANDARD; PRT; 8 AA.

RESULT 8
UH09_RAT
ID UH09_RAT STANDARD; PRT; 8 AA.
AC P56575;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Unknown protein from 2D-page of heart tissue (Spot P9) (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=Wistar; TISSUE=Heart;
RA Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,
RA Jungblut P.R.;
RL Submitted (SEP-1998) to the SWISS-PROT data bank.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 8.9, ITS MW IS: 42 kDa.
FT NON_TER 8
SQ SEQUENCE 8 AA; 1029 MW; 9E0775A6C4140B06 CRC64;

Query Match 18.3%; Score 21; DB 1; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.1e+05;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 16 QRETP 21
II I:
Db 3 RQSP 8

RESULT 9
UN41_CLOPA
ID UN41_CLOPA STANDARD; PRT; 13 AA.
AC P81360;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Unknown protein Cp 41 from 2D-page (Fragment).
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=W5;
RA Flengsrud R., Skjeldal L.;
RL "Two-dimensional gel electrophoresis separation and N-terminal
RT sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806(1998).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.6, ITS MW IS: 29.5 kDa.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1402 MW; 738AECF1E66CA2CB CRC64;

Query Match 18.3%; Score 21; DB 1; Length 13;
Best Local Similarity 27.3%; Pred. No. 1.9e+03;
Matches 3; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 YQTKVNLLSAI 11
II I:
Db 3 YSTEVSNNAGV 13

RESULT 10
CD4_SHEEP
ID CD4_SHEEP STANDARD; PRT; 20 AA.
AC P05542;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE T-cell surface glycoprotein CD4 (T-cell surface antigen T4/Leu-3)
DE (Fragment).
GN CD4.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE.
RX MEDLINE=86166694; PubMed=3082751;
RA Classon B.J., Tsagaratos J., Kirszbaum L., Maddox J., McKay C.R.,
RA Brandon M., McKenzie I.F.C., Walker I.D.;
RT "The L3T4 antigen in mouse and the sheep equivalent are
RT immunoglobulin-like.";
RL Immunogenetics 23:129-132(1986).
CC -!- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL
CC RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION.
CC -!- SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: TYPE I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
DR PIR: B47642; B47642.
KW Immunoglobulin domain; T-cell; Immune response.
FT NON_TER 20
SQ SEQUENCE 20 AA; 1928 MW; 421F09570FEA97EE CRC64;

Query Match 18.3%; Score 21; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 PCQ 16
III
Db 15 PCQ 17

RESULT 11
JHBP_BOMMO
ID JHBP_BOMMO STANDARD; PRT; 20 AA.
AC P81627;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Juvenile hormone-binding protein (Fragment).
DE JHBP.
GN Bombyx mori (Silk moth).
OS Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;
OC Ditrysia; Bombycoidea; Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE.
RC STRAIN=Backokjam; TISSUE=Hemolymph;
RA Park C.-H., Kim H.R.;
RT "Characterization of high affinity juvenile hormone binding protein in
RT the hemolymph of Bombyx mori L.";
RL Korean J. Zool. 37:495-503(1994).
RN [2]
RP IDENTIFICATION OF CVS-9.
RA Park C.-H.;
RL Submitted (DEC-1998) to the SWISS-PROT data bank.
CC -!- FUNCTION: PREVENTS JUVENILE HORMONE FROM BEING HYDROLYZED BY
```

CC GENERAL ESTERASES BY COMBINING WITH IT SPECIFICALLY.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 FT NON_TER 20
 SQ SEQUENCE 20 AA; 2090 MW; B336332F08AE2FB8 CRC64;

Query Match 18.3%; Score 21; DB 1; Length 20;
 Best Local Similarity 42.9%; Pred. No. 3e+03;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 10 AIKSPCQ 16
 I: ||:
 Db 4 ALLPCK 10

RESULT 12

ID COXM_RAT STANDARD; PRT; 10 AA.
 AC P80431;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Cytochrome c oxidase polypeptide VIIb, mitochondrial (EC 1.9.3.1)
 DE (Fragment).
 GN COX7B.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE.

RC STRAIN=Wistar; TISSUE=Liver;
 RX MEDLINE=9532429; PubMed=7601105;
 RA Schaeffer H., Noack H., Halangk W., Brandt U., von Jagow G.;
 RT "Cytochrome-c oxidase in developing rat heart. Enzymic properties and
 RT amino-terminal sequences suggest identity of the fetal heart and the
 RT adult liver isoform."
 RL Eur. J. Biochem. 230:235-241(1995).
 CC -1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
 CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
 CC MITOCHONDRIAL ELECTRON TRANSPORT.
 CC -1- CATALYTIC ACTIVITY: 4 ferrocycochrome c + O(2) = 4 ferricytochrome
 CC c + 2 H(2)O.
 KW Oxidoreductase; Mitochondrion.
 FT NON_TER 10
 SQ SEQUENCE 10 AA; 1210 MW; CFC70EB771A33326 CRC64;

Query Match 17.4%; Score 20; DB 1; Length 10;
 Best Local Similarity 60.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 16 QRETP 20
 I: ||:
 Db 3 QKKT 7

RESULT 13

ID ARCA_STRP5 STANDARD; PRT; 15 AA.
 AC P56827;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Arginine delminase (EC 3.5.3.6) (ADI) (Arginine dihydrolase) (AD)
 DE (Streptococcal acid glycoprotein) (Fragment).
 GN ARCA OR SAGP.
 OS Streptococcus pyogenes (serotype M5).
 CC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 CC Streptococcus.
 OX NCBI_TaxID=160491;
 RN [1]
 RP SEQUENCE, AND CHARACTERIZATION.
 RC STRAIN=Manfredo / Serotype M5;
 RX MEDLINE=98298018; PubMed=9632565;

RA Degnan B.A., Palmer J.M., Robson T., Jones C.E.D., Fischer M.,
 RA Glanville M., Mellor G.D., Diamond A.G., Kehoe M.A., Goodacre J.A.;
 RT "Inhibition of human peripheral blood mononuclear cell proliferation
 RT by Streptococcus pyogenes cell extract is associated with arginine
 RT delminase activity."
 RL Infect. Immun. 66:3050-3058(1998).
 CC -1- FUNCTION: Antitumor protein. Has a powerful and dose-dependent
 CC inhibitory effect on antigen, superantigen, or mitogen-stimulated
 CC human peripheral blood mononuclear cell (PBMC) proliferation. It
 CC may inhibit cell proliferation by arresting cell cycle and
 CC inducing apoptosis.
 CC -1- PATHWAY: Arginine degradation via arginine delminase; first step.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
 CC -1- SIMILARITY: BELONGS TO THE ARGinine DELMINASE FAMILY.
 KW Hydrolase; Arginine metabolism; Glycoprotein.
 FT INIT_MET 0
 FT NON_TER 15
 SQ SEQUENCE 15 AA; 1657 MW; D21150201B00EE46 CRC64;

Query Match 17.4%; Score 20; DB 1; Length 15;
 Best Local Similarity 40.0%; Pred. No. 3.2e+03;
 Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 QTKVNLISAI 11
 I: ||: ||:
 Db 3 QTPHVISEI 12

RESULT 14

ID CXA2_CONAL STANDARD; PRT; 15 AA.
 AC P56640;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Alpha-conotoxin AulB.
 OS Conus aulicus (Court cone).
 CC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 CC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=89437;
 RN [1]
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
 RC TISSUE=Venom;
 RX MEDLINE=99003392; PubMed=9786965;
 RA Luo S., Kulak J.M., Cartier G.E., Jacobsen R.B., Yoshikami D.,
 RA Olivera B.M., McIntosh J.M.;
 RT "Alpha-conotoxin AulB selectively blocks alpha3 beta4 nicotinic
 RT acetylcholine receptors and nicotine-evoked norepinephrine release."
 RL J. Neurosci. 18:8571-8579(1998).
 CC -1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
 CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
 CC INHIBIT THEM. THIS PEPTIDE BLOCKS MAMMALIAN NICOTINIC
 CC ACETYLCHOLINE RECEPTORS COMPOSED OF ALPHA-3/BETA-4 SUBUNITS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -1- MASS SPECTROMETRY: MW=1572.5; METHOD=Electrospray.
 CC -1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
 CC FAMILY.

CC Postsynaptic neurotoxin; Neurotoxin; Toxin;
 KW Acetylcholine receptor inhibitor; Amidation.
 FT DISULFID 2 8
 FT DISULFID 3 15
 FT MOD_RES 15 15
 SQ SEQUENCE 15 AA; 1578 MW; 84EFE95FDC700155 CRC64;
 AMIDATION.

Query Match 17.4%; Score 20; DB 1; Length 15;
 Best Local Similarity 37.5%; Pred. No. 3.2e+03;
 Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 14 PCQRETP 21
 I: ||:
 I: ||:

Db 7 PCFATNPD 14

RESULT 15

FIBA_CERSI
ID FIBA_CERSI STANDARD; PRT; 16 AA.
AC P14535;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Ceratotherium simum (White rhinoceros) (Square-lipped rhinoceros).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Rhinocerotidae; Ceratotherium.
OX NCBI_TaxID=9807;
RN [1]
RP SEQUENCE.
RA O'Neil P.B., Doolittle R.F.;
RT "Mammalian phylogeny based on fibrinopeptide amino acid sequences.";
RL Syst. Zool. 22:590-595(1973).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 16 FIBRINOPEPTIDE A.
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1639 MW; 0958CBB6293F4C81 CRC64;

Query Match 17.4%; Score 20; DB 1; Length 16;

Best Local Similarity 80.0%; Pred. No. 3.5e+03;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 18 ETPEG.22

|||

Db 2 ETTEG 6

Search completed: December 4, 2002, 13:36:48

Job time : 12 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 4, 2002, 13:35:15 ; Search time 28 seconds
(without alignments)
161.894 Million cell updates/sec

Title: US-09-754-004-2

Perfect score: 115

Sequence: 1 YQTKVNLSSAIKSPQRETPEG 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 7500

Minimum DB seq length: 0

Maximum DB seq length: 22

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	29	25.2	19	12	Q69267 equine herp
2	29	25.2	20	10	Q9S8M3 solanum tub
3	29	25.2	21	13	Q8UVD0 oreophasis
4	28	24.3	21	11	Q922Y9 mus musculu
5	27	23.5	20	6	Q9TRI0 bos taurus
6	27	23.5	22	4	Q96Q24 homo sapien
7	27	23.5	22	4	Q8TEZ8 homo sapien
8	26	22.6	14	9	Q9XJN4 bacterioph
9	26	22.6	17	4	Q9HB76 homo sapien
10	26	22.6	18	7	Q30216 homo sapien
11	26	22.6	20	4	Q16070 homo sapien
12	26	22.6	21	8	Q35556 pythium oli
13	25	21.7	18	15	Q41588 human immun
14	24	20.9	9	2	Q9R792 borrelia bu
15	24	20.9	9	2	Q9R3T0 borrelia af
16	24	20.9	10	2	Q9R791 borrelia af

17	24	20.9	11	2	Q9R790	Q9r790 borrelia ga
18	24	20.9	16	6	O77491	O77491 nycticebus
19	24	20.9	17	10	Q9SMC7	Q9smc7 lycopersico
20	24	20.9	18	4	Q16167	Q16167 homo sapien
21	24	20.9	19	15	Q905F2	Q905f2 human immun
22	24	20.9	21	5	P82308	P82308 maia squina
23	23	20.0	13	3	Q96VH7	Q96vh7 geotrichum
24	23	20.0	19	2	Q9K4X0	Q9k4x0 planktothri
25	23	20.0	19	11	Q9JK02	Q9jk02 mus musculu
26	23	20.0	19	15	Q905I8	Q905i8 human immun
27	23	20.0	19	15	Q905H6	Q905h6 human immun
28	23	20.0	19	15	Q905E0	Q905e0 human immun
29	23	20.0	20	10	P82940	P82940 hordeum vul
30	23	20.0	20	11	Q9QVG0	Q9qvg0 rattus sp.
31	23	20.0	21	2	O51540	O51540 pseudomonas
32	23	20.0	22	11	Q9WUK1	Q9wuk1 rattus norv
33	23	20.0	22	16	Q9JYP0	Q9jyp0 neisseria m
34	22	19.1	11	4	O75811	O75811 homo sapien
35	22	19.1	12	2	Q46712	Q46712 escherichia
36	22	19.1	12	8	Q8SLF4	Q8slf4 taraxacum (
37	22	19.1	12	11	Q90ZY4	Q9qzy4 mus musculu
38	22	19.1	13	8	Q8SLF7	Q8slf7 taraxacum (
39	22	19.1	13	11	O54809	O54809 mus musculu
40	22	19.1	14	4	Q16332	Q16332 homo sapien
41	22	19.1	15	4	Q93046	Q93046 homo sapien
42	22	19.1	15	4	Q9UCH4	Q9uch4 homo sapien
43	22	19.1	15	8	Q8SLG7	Q8slg7 taraxacum (
44	22	19.1	15	8	Q8SLF5	Q8slf5 taraxacum (
45	22	19.1	16	8	Q95AY0	Q95ay0 artemisia r

ALIGNMENTS

RESULT 1

Q69267 ID Q69267 PRELIMINARY; PRT; 19 AA.
AC Q69267;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Hypothetical 2.1 kDa protein.
GN IE.
OS Equine herpesvirus 1.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=10326;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KENTUCKY A;
RX MEDLINE=90064773; PubMed=2555546;
RA Harty R.N., Colle C.F., Grundy F.J., O'Callaghan D.J.;
RT "Mapping the termini and intron of the spliced immediate-early
transcript of equine herpesvirus 1.";
RL J. Virol. 63:5101-5110(1989).
DR EMBL: M30497; AAA66551.1; -;
KW Hypothetical protein.
SQ SEQUENCE 19 AA; 2067 MW; E920FDB48CC97CC9 CRC64;

Query Match 25.2%; Score 29; DB 12; Length 19;
Best Local Similarity 55.6%; Pred. No. 5.3e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 14 PCQRETPEG 22
| | | | |
Db 3 PLQQRCPPEG 11

RESULT 2

Q9S8M3 ID Q9S8M3 PRELIMINARY; PRT; 20 AA.
AC Q9S8M3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)

```
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE PSEUDOTHIONIN-ST1 (Fragment).
OS Solanum tuberosum (potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RX SEQUENCE.
RX MEDLINE=94307252; PubMed=8033886;
RA Moreno M., Segura A., Garcia-Olmedo F.;
RA "Pseudothionin-St1, a potato peptide active against potato
RT pathogens.";
RL Eur. J. Biochem. 223:135-139(1994).
DR InterPro; IPR002118; Gamma-thionin.
DR Pfam; PF00304; Gamma-thionin; 1.
SQ SEQUENCE 20 AA; 2311 MW; EFF9D90708DF2F9D CRC64;

Query Match 25.2%; Score 29; DB 10; Length 20;
Best Local Similarity 35.7%; Pred. No. 5.6e+02;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 6 NLLSAIKSPCQRET 19
   :| | | | |
Db 5 SLSHRFKGPCTRDS 18

RESULT 3
Q8UVD0 PRELIMINARY; PRT; 21 AA.
AC Q8UVD0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Chrom-domain-helicase-DNA-binding protein 1 (Fragment).
OS Oreophasis derbianus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Cracidae; Oreophasis.
OX NCBI_TaxID=125067;
RN [1]
RX SEQUENCE FROM N.A.
RA Chavez-Zamarrilla P., Bermudez-Humaran L.G., Guzman-Velasco A.,
RA Leal-Garza C.H., Montes de Oca-Luna R.;
RT "Lost of restriction site Ddel, used for avian molecular sexing, in
RT Oreophasis derbianus.";
RL Reprod. Domest. Anim. 0:0-0(2002).
DR EMBL; AF462044; AAL69358.1; -.
KW Helicase; DNA-binding.
FT NON_TER 1
FT NON_TER 21
SQ SEQUENCE 21 AA; 2522 MW; 3C139D112DDF2A0E CRC64;

Query Match 25.2%; Score 29; DB 13; Length 21;
Best Local Similarity 50.0%; Pred. No. 5.9e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 14 PCQRETP 21
   |||:| |
Db 1 PCQKENDQ 8

RESULT 4
Q922Y9 PRELIMINARY; PRT; 21 AA.
AC Q922Y9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Unknown (protein for MGC:7898).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
..
```

```
OX NCBI_TaxID=10090;
RN [1]
RX SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006692; AAH06692.1; -.
SQ SEQUENCE 21 AA; 2315 MW; 60698D703D0C1692 CRC64;

Query Match 24.3%; Score 28; DB 11; Length 21;
Best Local Similarity 46.2%; Pred. No. 8.8e+02;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 TKVNLSSAIKSPC 15
   |::|| |
Db 8 TALHLLPRGSSPC 20

RESULT 5
Q9TRI0 PRELIMINARY; PRT; 20 AA.
AC Q9TRI0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Pre-alpha-trypsin inhibitor HC3 component homolog (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RX SEQUENCE.
RX MEDLINE=93178646; PubMed=7680011;
RA Castillo G.M., Templeton D.M.;
RT "Subunit structure of bovine ESF (extracellular-matrix stabilizing
RT factor(s)). A chondroitin sulfate proteoglycan with homology to human
RT I alpha 1 (inter-alpha-trypsin inhibitors).";
RL FEBS Lett. 318:292-296(1993).
SQ SEQUENCE 20 AA; 2143 MW; B2A6EB2B4AA76BE9 CRC64;

Query Match 23.5%; Score 27; DB 6; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YQTKVN 6
   | | | |
Db 13 YSTKVN 18

RESULT 6
Q96Q24 PRELIMINARY; PRT; 22 AA.
AC Q96Q24;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Mitochondrial ribosomal protein S23 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RX SEQUENCE FROM N.A.
RX MEDLINE=21429115; PubMed=11543634;
RA Kenmochi N., Suzuki T., Uechi T., Magoori M., Kuniba M., Higa S.,
RA Watanabe K., Tanaka T.;
RT "The human mitochondrial ribosomal protein genes: Mapping of 54 genes
RT to the chromosomes and implications for human disorders.";
RL Genomics 77:65-70(2001).
DR EMBL; AB061206; BAB54956.1; -.
KW Ribosomal protein.
FT NON_TER 1
FT NON_TER 1
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FT NON_TER 22 22
SQ SEQUENCE 22 AA; 2536 MW; A079BB04B5E5F7A6 CRC64;

Query Match 23.5%; Score 27; DB 4; Length 22;
Best Local Similarity 83.3%; Pred. No. 1.4e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 KSPCQR 17
Db 17 KSTCQR 22

RESULT 7

ID Q8TEZ8 PRELIMINARY; PRT; 22 AA.
AC Q8TEZ8;
DT 01-JUN-2002 (T-EMBLrel. 21, Created)
DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
DE 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
DE Spinocerebellar ataxia type 7 (Fragment).
GN SCA7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Elum D.D., Clark A.M., Gouw L.G., Ptacek L.J., Fu Y.-H.;
RT "The product of a novel SCA7 splice variant is enriched within the
central nervous system."
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF32956; AAL79807.1; -.
FT NON_TER 1
FT NON_TER 22
SQ SEQUENCE 22 AA; 2273 MW; B2F9FB5DE040C571 CRC64;

Query Match 23.5%; Score 27; DB 4; Length 22;
Best Local Similarity 71.4%; Pred. No. 1.4e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 11 IKSPCQR 17
Db 2 ISSPCLR 8

RESULT 8

ID Q9XJN4 PRELIMINARY; PRT; 14 AA.
AC Q9XJN4;
DT 01-NOV-1999 (T-EMBLrel. 12, Created)
DT 01-NOV-1999 (T-EMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DE P10 (Fragment).
OS bacteriophage phi-9.
OC Viruses; dsRNA viruses; Cystoviridae; Cystovirus.
OX NCBI_TaxID=90887;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99350412; PubMed=10419946;
RA Mindich L., Qiao X., Qiao J., Onodera S., Romantschuk M.,
RA Hoogstraten D.;
RT "Isolation of additional bacteriophages with genomes of segmented
double-stranded RNA."
RL J. Bacteriol. 181:4505-4508(1999).
DR EMBL; AF125678; AAD22559.1; -.
FT NON_TER 14
SQ SEQUENCE 14 AA; 1548 MW; 21AF9FA6CFD80E37 CRC64;

Query Match 22.6%; Score 26; DB 9; Length 14;
Best Local Similarity 44.4%; Pred. No. 1.3e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 NLSAISKSP 14

Db 3 NILDPLKAP 11

RESULT 9

ID Q9HB76 PRELIMINARY; PRT; 17 AA.
AC Q9HB76;
DT 01-MAR-2001 (T-EMBLrel. 16, Created)
DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DE Arginine vasopressin (Fragment).
GN AVP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lin M.T., Wang N., Chen Y.C., Fang L., Wu Z.Y., Murong S.X.;
RT "A GAG deletion within two consecutive GAG sequences in exon 2 of the
arginine vasopressin gene in Chinese."
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF272848; AAG16747.1; -.
FT HSSP; P01180; INPO.
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 1923 MW; 7EFD60BD634B6B15 CRC64;

Query Match 22.6%; Score 26; DB 4; Length 17;
Best Local Similarity 66.7%; Pred. No. 1.6e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 IKSPCQ 16
Db 12 LPSPCQ 17

RESULT 10

ID Q30216 PRELIMINARY; PRT; 18 AA.
AC Q30216;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DE Human leukocyte antigen alpha chain (Fragment).
GN HLA DOAI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95084785; PubMed=7974465;
RA Fogdell A., Olerup O.;
RT "The DOAI*0104 allele is carried by DRB1*1001- and DRB1*1401-positive
haplotypes in Caucasians, Africans and Orientals."
RL Tissue Antigens 44:19-24(1994).
DR EMBL; S75685; AAB32621.1; -.
FT NON_TER 1
SQ SEQUENCE 18 AA; 1708 MW; 097492525C2252FC CRC64;

Query Match 22.6%; Score 26; DB 7; Length 18;
Best Local Similarity 45.5%; Pred. No. 1.7e+03;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 8 LSAIKSPCQRE 18
Db 5 LTTWMSPCGGE 15

RESULT 11

Q16070

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ID Q16070 PRELIMINARY; PRT; 20 AA.
AC Q16070;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Neurofilament heavy subunit (Fragment).
GN NEFH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94040777; PubMed=8224877;
RA Figlewicz D.A., Rouleau G.A., Krizus A., Julien J.P.;
RT "Polymorphism in the multi-phosphorylation domain of the human
RT neurofilament heavy-subunit-encoding gene.";
RL Gene 132:297-300(1993).
DR EMBL; S66488; AAB28609.1; -.
FT NON_TER 1
SQ SEQUENCE 20 AA; 2198 MW; E9A0975B41FD8082 CRC64;

Query Match 22.6%; Score 26; DB 4; Length 20;
Best Local Similarity 50.0%; Pred. No. 1.9e+03;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 12 KSPCORETPE 21
   ||| : :||
Db 6 KSPERAKSPE 15

RESULT 12
Q35556 PRELIMINARY; PRT; 21 AA.
AC Q35556;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 2.5 kDa protein.
OS Pythium oligandrum.
OG Mitochondrion.
OC Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae; Pythium.
OX NCBI_TaxID=41045;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17-1;
RA Martin F.N.;
RT "Linear mitochondrial genome organization in vivo in the genus
RT Pythium.";
RL Curr. Genet. 27:0-0(1995).
DR EMBL; U28355; AAA70034.1; -.
KW Hypothetical protein; Mitochondrion.
SQ SEQUENCE 21 AA; 2491 MW; 883B7AB7A5D4445E CRC64;

Query Match 22.6%; Score 26; DB 8; Length 21;
Best Local Similarity 83.3%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 KVNLLS 9
   | :|||
Db 15 KINLLS 20

RESULT 13
O41588 PRELIMINARY; PRT; 18 AA.
ID O41588;
AC O41588;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE "Envelope glycoprotein (Fragment).
DE ENV".
OS Human immunodeficiency virus type 1."

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OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PC13;
RX MEDLINE=98105804; PubMed=9445059;
RA Connor R.I., Korber B.T.M., Graham B.S., Hahn B.H., Ho D.D.,
RA Walker B.D., Neumann A.U., Vermund S.H., Mestecky J., Jackson S.,
RA Fenamore E., Cao Y., Gao F., Kalams S., Kunstman K.J., McDonald D.,
RA McWilliams N., Trkola A., Moore J.P., Wolinsky S.M.;
RT "Immunological and virological analyses of persons infected by human
RT immunodeficiency virus type 1 while participating in trials of
RT recombinant gp120 subunit vaccines.";
RL J. Virol. 72:1552-1576(1998).
DR EMBL; U84837; AAC58876.1; -.
KW AIDS; Coat protein; Glycoprotein.
FT NON_TER 1
SQ SEQUENCE 18 AA; 2050 MW; 656402FB0913D46E CRC64;

Query Match 21.7%; Score 25; DB 15; Length 18;
Best Local Similarity 57.1%; Pred. No. 2.5e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 14 PCQRETP 20
   || : ||
Db 2 PCVKLTP 8

RESULT 14
Q9R792 PRELIMINARY; PRT; 9 AA.
ID Q9R792;
AC Q9R792;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Outer surface protein C (Fragment).
GN OSPC.
OG Spirochaetales; Spirochaetaceae; Borrelia.
OC Borrelia burgdorferi (Lyme disease spirochete).
OX Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B31;
RX MEDLINE=97426044; PubMed=9282748;
RA Tilly K., Casjens S., Stevenson B., Bono J.L., Samuels D.S., Hogan D.,
RA Rosa P.;
RT "The Borrelia burgdorferi circular plasmid cp26: conservation of
RT plasmid structure and targeted inactivation of the ospC gene.";
RL Mol. Microbiol. 25:361-374(1997).
DR EMBL; U93693; AAC45521.1; -.
DR InterPro; IPR001800; Lipoprotein_6.
DR Pfam; PF01441; Lipoprotein_6; 1.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1005 MW; 4864C5B731A44333 CRC64;

Query Match 20.9%; Score 24; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 6.7e+05;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

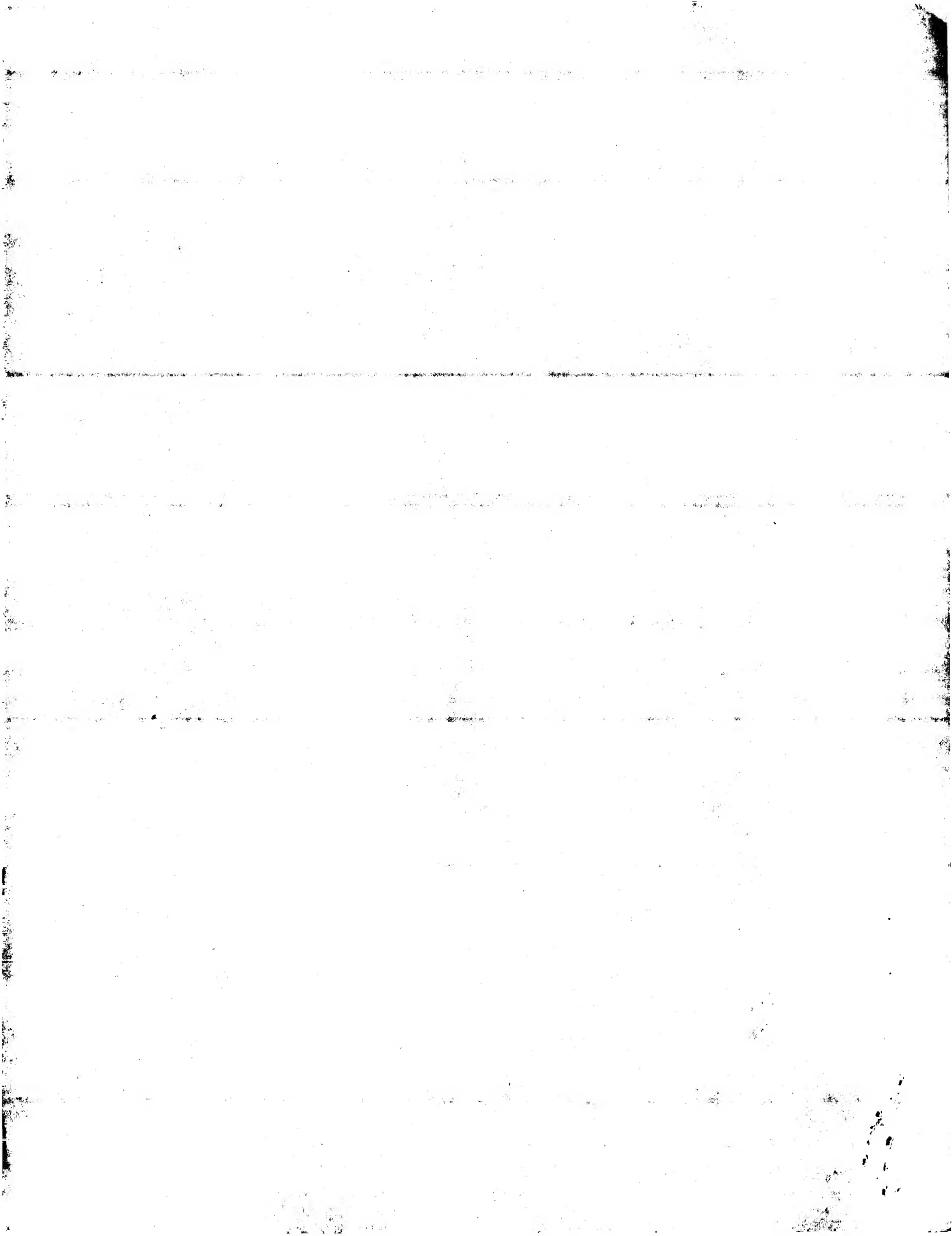
QY 4 KVNLLSAI 11
   | | | | |
Db 2 KKNTLSAI 9

RESULT 15
Q9R3T0 PRELIMINARY; PRT; 9 AA.
ID Q9R3T0;
AC Q9R3T0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Outer surface protein C (Fragment).
GN OSPC.

```

OS Borrelia afzelii.
 OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
 OX NCBI_TaxID=29518;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PKO, IP21, AND J1;
 RX MEDLINE=97426044; PubMed=9282748;
 RA Tilly K., Casjens S., Stevenson B., Bono J.L., Samuels D.S., Hogan D.,
 RA Rosa P.;
 RT "The Borrelia burgdorferi circular plasmid cp26: conservation of
 RT plasmid structure and targeted inactivation of the ospC gene."
 RL Mol. Microbiol. 25:361-374(1997).
 DR EMBL; U93698; AAC45531.1; -.
 DR EMBL; U93696; AAC45527.1; -.
 DR EMBL; U93697; AAC45529.1; -.
 DR InterPro: IPR001800; Lipoprotein_6.
 DR Pfam: PF01441; Lipoprotein_6; 1.
 FT NON_TER
 SQ SEQUENCE 9 AA: 1005 MW: 48645B731A44333 CRC64;
 Query Match 20.9%; Score 24; DB 2; Length 9;
 Best Local Similarity 75.0%; Pred. No. 6.7e+05;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 4 KVNLLSAI 11
 Db 2 KKNTLSAI 9

Search completed: December 4, 2002, 13:37:24
 Job time : 29 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 4, 2002, 13:32:34 ; Search time 35 Seconds
(without alignments)
83.758 Million cell updates/sec

Title: US-09-754-004-2

Perfect score: 115

Sequence: 1 YQKVNLLSAIKSPQRETPEG 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 303745

Minimum DB seq length: 0

Maximum DB seq length: 22

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	115	100.0	22	AAW22950	hTNF-alpha epitope
2	115	100.0	22	AAW59149	Human tumour necro
3	67	58.3	22	AAW05485	Tumour necrosis fa
4	63	54.8	17	AAAB11028	Immunogenic peptid
5	48	41.7	17	AAAB05469	Tumour necrosis fa
6	41	35.7	14	AAAY90384	Tumour necrosis fa
7	40	34.8	22	AAAR67688	h-TNF (73-94). Sy
8	38	33.0	14	AAAR06772	Tumour necrosis fa
9	38	33.0	14	AAAY82194	Tumour necrosis fa
10	38	33.0	17	AAAG60233	hTNF-alpha tip. S

11	38	33.0	17	21	AAAY82196	Tumour necrosis fa
12	37	32.2	15	22	AAAG64014	Human cytochrome C
13	36	31.3	17	22	ABB33440	Peptide #946 enco
14	36	31.3	17	22	ABB18899	Protein #898 enco
15	36	31.3	17	22	AAW54225	Human brain expres
16	36	31.3	17	22	AAW66619	Human bone marrow
17	36	31.3	17	22	AAW14492	Peptide #926 enco
18	36	31.3	17	22	AAW26905	Peptide #942 enco
19	36	31.3	17	22	AAW02219	Peptide #901 enco
20	36	31.3	17	23	ABG36271	Human peptide enco
21	34	29.6	15	14	AAAR38560	Sequence of peptid
22	34	29.6	15	18	AAW12205	Tolerogenic peptid
23	34	29.6	15	19	AAW85274	Helper T-cell pept
24	34	29.6	15	19	AAW85281	Helper T-cell pept
25	34	29.6	15	22	AAJ03092	Hepatitis C virus
26	34	29.6	15	22	AAJ03149	Hepatitis C virus
27	34	29.6	15	22	AAJ03168	Hepatitis C virus
28	34	29.6	15	22	AAJ03255	Hepatitis C virus
29	34	29.6	15	22	AAJ03398	Hepatitis C virus
30	34	29.6	15	22	AAJ03456	Hepatitis C virus
31	34	29.6	15	22	AAJ03475	Hepatitis C virus
32	34	29.6	15	22	AAJ03560	Hepatitis C virus
33	34	29.6	15	22	AAJ03645	Hepatitis C virus
34	34	29.6	20	23	AAE21999	Hepatitis C virus
35	33	28.7	8	22	AAU69056	Bacterial conserve
36	33	28.7	16	17	AAAR9385	Human REST protein
37	33	28.7	19	22	ABB37772	Peptide #5278 enco
38	33	28.7	19	22	ABB20613	Protein #2612 enco
39	33	28.7	19	22	AAW58385	Human brain expres
40	33	28.7	19	22	AAW70869	Human bone marrow
41	33	28.7	19	22	AAW18710	Peptide #5144 enco
42	33	28.7	19	22	AAW31162	Peptide #5199 enco
43	33	28.7	19	23	ABG37943	Human peptide enco
44	32	27.8	9	21	AAV86759	Telomerase peptid
45	32	27.8	19	21	AAAY91660	Human secreted pro

ALIGNMENTS

RESULT 1

AAW22950
ID AAW22950 standard; peptide; 22 AA.

XX AC AAW22950;

XX DT 05-MAR-1998 (first entry)

XX DE hTNF-alpha epitope 87-108.

XX KW tumour necrosis factor alpha; TNF; epitope; antibody; antagonist;
fibrinogen; cardiovascular; cerebrovascular; thrombosis; stroke;
thrombophlebitis; myocardial infarction; embolism; ischaemia.

XX OS Homo sapiens.

XX OS OS

XX PN WO9730088-A2.

XX PD 21-AUG-1997.

XX PF 17-FEB-1997; 97WO-GB00435.

XX PR 16-FEB-1996; 96US-0602272.

XX PA (KENN-) KENNEDY INST RHEUMATOLOGY.

XX PI Elliott MJH, Feldmann M, Maini RN;

XX DR WPI; 1997-424980/39.

XX PT Treating and preventing cardiovascular, cerebrovascular or
thrombotic disorder, or decreasing plasma fibrinogen - by
administration of tumour necrosis factor antagonist

XX PS Claim 10; Page 14; 57pp; English.

XX CC The invention relates to the use of an antagonist of tumour necrosis

XX CC factor (TNF) for the treatment of vascular disease, cardiovascular

XX CC disorders, thrombotic disorders, or illnesses or pathologies which

XX CC are treatable by decreasing plasma fibrinogen. Typical conditions which

XX CC can be treated include acute myocardial infarction, deep vein thrombosis,

XX CC thrombophlebitis, stroke, thromboembolic disorder or ischemic events.

XX CC In one embodiment the antagonist used is an anti-TNF antibody

XX CC (optionally chimeric, humanised or resurfaced), preferably one which

XX CC binds to an epitope comprising at least 5 amino acids within the region

XX CC TNF-alpha 87-108 and/or TNF-alpha 59-80. The present sequence represents

XX CC the 87-108 epitope.

XX SQ Sequence 22 AA;

Query Match 100.0%; Score 115; DB 18; Length 22;

Best Local Similarity 100.0%; Pred. No. 4.1e-12;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YOTKVNLLSAIKSPCQRETPEG 22

Db 1 YOTKVNLLSAIKSPCQRETPEG 22

|||||

RESULT 2

AAW59149

ID AAW59149 standard; peptide; 22 AA.

AC AAW59149;

XX DT 13-AUG-1998 (first entry)

XX DE Human tumour necrosis factor-alpha epitope pos. 87-108.

XX KW Tumour necrosis factor-alpha; epitope; human immunodeficiency virus;

XX KW HIV; TNF-alpha; anti-TNF; antibody; treatment; prevention; infection;

XX KW acquired immune deficiency disease; interleukin-2; IL-2; gene therapy;

XX KW systemic toxicity; CD4+ cell; inflammation; immune response.

XX OS Homo sapiens.

XX PN WO9811917-A1.

XX PD 26-MAR-1998.

XX PF 17-SEP-1997; 97WO-US16116.

XX PR 19-SEP-1996; 96US-0716107.

XX PA (CENZ) CENTOCOR INC.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI McCloskey RV, Walker RE, Woody JN;

XX WPI; 1998-230303/20.

XX PT Treating or preventing acquired immune deficiency syndrome using

XX PT interleukin-2 - and antibodies against tumour necrosis factor, to

XX PT reduce side effects of the treatment

XX PS Claim 10; Page 11; 50pp; English.

XX CC This peptide sequence is a fragment of tumour necrosis factor-alpha

XX CC (TNF-alpha) corresponding to amino acid position 87-108 of the full

XX CC length protein. This region is an epitope and is recognized and/or binds

XX CC with anti-TNF activity. This fragment is used to describe a novel method

XX CC of treating or preventing acquired immune deficiency disease and

XX CC infection with human immune deficiency virus (HIV) by co-administration

XX CC of interleukin-2 (IL-2) and a chimeric antibody (Ab), or its fragment,

XX CC against tumour necrosis factor (TNF). IL-2 and Ab are administered by

XX CC infection, orally, topically or are produced from gene therapy vectors,

CC but preferably by intravenous injection or infusion. Usual doses are

CC 0.01-100 (especially 1-40) mg/kg/day, in 1-6 portions or in sustained

CC release form. Further doses may be given, just before or during relapse.

CC Inhibition of TNF alpha by Ab alleviates some of the systemic toxicity

CC associated with administration of IL-2 (which increases the level of CD4+

CC cells but also stimulates production of TNF, high levels of which cause

CC unwanted inflammatory and immunological responses). Blockade of TNF

CC allows administration of higher doses of IL-2 than would be otherwise

CC possible.

XX SQ Sequence 22 AA;

Query Match 100.0%; Score 115; DB 19; Length 22;

Best Local Similarity 100.0%; Pred. No. 4.1e-12;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YOTKVNLLSAIKSPCQRETPEG 22

Db 1 YOTKVNLLSAIKSPCQRETPEG 22

|||||

RESULT 3

AAW05485

ID AAR05485 standard; protein; 22 AA.

XX AC AAR05485;

XX DT 23-OCT-1990 (first entry)

XX DE Tumour necrosis factor derived peptide.

XX KW Tumour necrosis factor; TNF; neoplastic disease; autoimmune

XX KW disease; infection; inflammation; transplant rejection.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Disulfide-bond 5..18

FT Modified-site 5..5

FT Modified-site /label-Hcy

FT Modified-site 18..18

FT /label-Hcy

XX PN DE3841759-A.

XX PD 13-JUN-1990.

XX PF 12-DEC-1988; 88DE-3841759.

XX PR 12-DEC-1988; 88DE-3841759.

XX PA (BADI) BASF AG.

XX PI Bohm HJ, Daum L, Haupt A, Schmied B, Walker N, Zechel JC;

XX WPI; 1990-186576/25.

XX PT New tumour necrosis factor derived peptides- for treating or preventing

XX PT neoplastic and autoimmune diseases, infection, inflammation and

XX PT transplant rejection.

XX PS Example 24; Page 9; 16pp; German.

XX CC To residue 11 is attached Ac and to residue 122 NH2.

XX CC This peptide is an example of a highly generic sequence of the

XX CC formula X-A-Y.

XX CC A= QRETPGEAEAKP, HRETPEAEAKP, PRDTPGEAEAKP, PGLOEP,

XX CC PGQGP or PGLOQP;

XX CC X= G-NH-CHM-CO, G-NH-CHM-CO-W, G-R-NH-CHM-CO-W;

XX CC Y= Z, NH-CHO-COZ, V-NH-CHO-COZ, NH-CHO-CO-U-Z or V-NH-CHO-CO-U-Z;

XX CC G= H or an amino protecting group;

XX CC Z= OH, NH2 or carboxy protecting group; or G and Z together are a

XX CC covalent bond or the gp. CO(CH2)anH; a=1-12;

CC R, U, V and W= peptide chains of 1-4 naturally occurring alpha aminoacids;
 CC M and O= H, isopropyl, CHMe.Et, phenyl, CH(OH), 3-indolyl- or
 CC 4-imidazolyl-methyl or (CH2)BT; b=1-6;
 CC T= OH, MeO, MeS, isopropyl, phenyl (opt. 4-OH, substd.), HS, NH2, COOH,
 CC CONH2, or NH2 C (NH) NH; or
 CC M ans Q together are (CH2)c-S-S-(CH2)d, (CH2)eCO NH-(CH2)f or
 CC (CH)2eNH CO(CH2)gNH CO(CH2) f; c and d=1-4; e and f=1-6; g=1-12.
 CC The peptide is a low mol. wt. deriv. of TNF.
 CC See also DE3841753-55, DE3841759, DE3841761-64, DE3841767-68.
 XX
 SQ Sequence 22 AA;

Query Match 58.3%; Score 67; DB 11; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.00041;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 IKSPCQRETPEG 22
 Db 1 IKSPCQRETPEG 12
 |||||

RESULT 4
 AAB11028
 ID AAB11028 standard; peptide; 17 AA.
 XX
 AC AAB11028;

DT 08-FEB-2001 (first entry)

XX Immunogenic peptide #2 for raising human TNF-alpha antigen.

XX Immunogenic; antigen; C3a; C5a; IL10; IL1-alpha; IL1-beta; IL6;
 KW TNF-alpha; immunoadsorber; treatment; sepsis; complement factor;
 KW anti-inflammatory; antiseptis; plasmapheresis; septic shock.

XX Homo sapiens.

XX DE19913707-A1.

PD 05-OCT-2000.

XX 26-MAR-1999; 99DE-1013707.

XX 26-MAR-1999; 99DE-1013707.

XX (PRIV-) PRIVATES INST BIOSERV GMBH.

XX Heinrich H, Hahn H, Meyer U, Kruschke P, Wagner H;

XX WPI; 2000-648176/63.

XX Immunoadsorber for treating sepsis, comprises polymeric support
 PT carrying antibodies specific for complement factors and
 PT lipopolysaccharide

XX Example 1; Page 4; 8pp; German.

XX This invention describes a novel immunoadsorber (A) for treating sepsis
 CC which comprises a carrier of organic or synthetic polymer having bound to
 CC it poly- or monoclonal antibodies (Ab1) against the complement factors
 CC C3a and/or C5a and against lipopolysaccharide (LPS). Optionally other
 CC antibodies (Ab2) directed against other mediators of sepsis are also
 CC attached to the carrier. The products of the invention have
 CC anti-inflammatory and antiseptis activity. (A) are used for treatment,
 CC particularly by plasmapheresis, of sepsis and septic shock. The
 CC combination of antibodies used can be tailored to the requirements of
 CC individual patients.

XX Sequence 17 AA;

Query Match 54.8%; Score 63; DB 21; Length 17;
 Best Local Similarity 100.0%; Pred. No. 0.0014;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 KSPCQRETPEG 22
 Db 1 KSPCQRETPEG 11
 |||||

RESULT 5
 AAR05469
 ID AAR05469 standard; protein; 17 AA.
 XX
 AC AAR05469;

DT 23-OCT-1990 (first entry)

XX Tumour necrosis factor derived peptide.

XX Tumour necrosis factor; TNF; neoplastic disease; autoimmune
 KW disease; infection; inflammation; transplant rejection.

XX Synthetic.

XX DE3841759-A.

XX 13-JUN-1990.

XX 12-DEC-1988; 88DE-3841759.

XX 12-DEC-1988; 88DE-3841759.

XX (BADI) BASF AG.

XX Bohm HJ, Daum L, Haupt A, Schmied B, Walker N, Zechel JC;

XX WPI; 1990-186576/25.

XX New tumour necrosis factor derived peptides- for treating or preventing
 PT neoplastic and autoimmune diseases, infection, inflammation and
 PT transplant rejection.

PS Example 1; Page 7; 16pp; German.

XX To residue S1 is attached Ac and to residue T17 NH2.

CC This peptide is an example of a highly generic sequence of the
 CC formula X-A-Y.

CC A= QRETPGEAEAKP, HRETPWEAEAKP, HRETPGEAEAPNA, PROTPGEAEALKP, PGLQEP,
 CC PGPQGP or PGLOGP;

CC X= G-NH-CHM-CO, G-NH-CHM-CO-W, G-R-NH-CHM-CO or G-R-NH-CHM-CO-W;
 CC Y= Z, NH-CHQ-COZ, V-NH-CHQ-COZ, NH-CHQ-CO-U-Z or V-NH-CHQ-CO-U-Z;

CC G= H or an amino protecting group;

CC Z= OH, NH2 or carboxy protecting group; or G and Z together are a
 CC covalent bond or the gp. CO(CH2)ANH; a=1-12;

CC R, U, V and W= peptide chains of 1-4 naturally occurring alpha aminoacids;

CC M and Q= H, isopropyl, CHMe.Et, phenyl, CH(OH), 3-indolyl- or
 CC 4-imidazolyl-methyl or (CH2)BT; b=1-6;

CC T= OH, MeO, MeS, isopropyl, phenyl (opt. 4-OH, substd.), HS, NH2, COOH,
 CC CONH2, or NH2 C (NH) NH; or

CC M ans Q together are (CH2)c-S-S-(CH2)d, (CH2)eCO NH-(CH2)f or
 CC (CH)2eNH CO(CH2)gNH CO(CH2) f; c and d=1-4; e and f=1-6; g=1-12.

CC The peptide is a low mol. wt. deriv. of TNF.

CC See also DE3841753-55, DE3841759, DE3841761-64, DE3841767-68.

XX Sequence 17 AA;

Query Match 41.7%; Score 48; DB 11; Length 17;
 Best Local Similarity 90.0%; Pred. No. 0.44;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 SPCQRETPEG 22
 Db 1 SPTQRETPEG 10
 |||||

RESULT 6

```

AA90384
ID AAY90384 standard; peptide; 14 AA.
XX
AC AAY90384;
XX
DT 15-JAN-2001 (first entry)
XX
DE Tumour necrosis factor inhibitor peptide #110.
XX
KW Tumour necrosis factor; inhibitor; TNF-alpha; TNF p55 receptor; cachexia;
KW TNF p75 receptor; sepsis syndrome; circulatory collapse; infection;
KW immune disorder; autoimmune disorder; systemic lupus erythematosus;
KW rheumatoid arthritis; alcohol-induced hepatitis; inflammatory disorder;
KW sarcoidosis; Crohn's disease; vascular inflammatory disease; therapy;
KW disseminated intravascular coagulation; graft-versus-host disease;
KW Rawasaki's disease; malignant disorder; TNF-alpha-secreting tumour.
XX
OS Synthetic.
XX
US6107273-A.
XX
PD 22-AUG-2000.
XX
PF 24-JAN-1995; 95US-0377781.
XX
PR 24-JAN-1995; 95US-0377781.
XX
PA (UYJE-) UNIV JEFFERSON THOMAS.
XX
PI Jameson BA, Noe M;
XX
DR WPI; 2000-571331/53.
XX
PT Novel tumor necrosis factor inhibitors for treating disorders mediated
PT by tumor necrosis factor alpha activity e.g. autoimmune disorders,
PT pathogenic infections, malignant tumors and cachexia -
XX
PS Claim 18; Column 28; 17pp; English.
XX
CC This sequence represents a fragment of a tumour necrosis factor inhibitor
CC of the invention. The inhibitors are antagonists of tumour necrosis
CC factor-alpha (TNF-alpha), comprising less than 15 amino acids, having
CC restricted conformation and capable of binding to TNF p55 and/or TNF p75
CC receptor. The inhibitors are useful for treating a disease or condition
CC mediated by TNF-alpha such as sepsis syndrome, cachexia, circulatory
CC collapse and shock resulting from acute or chronic bacterial infection;
CC acute and chronic parasitic or infectious processes, including bacterial,
CC viral and fungal infections; acute and chronic immune and autoimmune
CC disorder, such as systemic lupus erythematosus and rheumatoid arthritis,
CC alcohol-induced hepatitis; chronic inflammatory disorder such as
CC sarcoidosis and Crohn's disease; vascular inflammatory disorder such as
CC disseminated intravascular coagulation, graft-versus-host disease,
CC Rawasaki's disease, and malignant disorders involving TNF-alpha-secreting
CC tumours.
XX
SQ Sequence 14 AA;
Query Match 35.7%; Score 41; DB 21; Length 14;
Best Local Similarity 87.5%; Pred. No. 5.2;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 15 CORETPEG 22
Db 1 CPRETPEG 8
RESULT 7
AAR87688
ID AAR87688 standard; peptide; 22 AA.
XX
AC AAR87688;
XX
DT 10-MAY-1996 (first entry)
XX

```

```

XX
DE h-TNF (73-94).
XX
KW TNF; tumour necrosis factor; neutrophil; superoxide; inflammation;
KW AIDS, cancer; rheumatoid arthritis; ARDS; cystic fibrosis;
KW tuberculosis; TB; Crohn's disease; sarcoidosis; leprosy; syphilis;
KW malaria; adult respiratory distress syndrome.
XX
OS Synthetic.
XX
PN AU9344664-A.
XX
PD 02-MAR-1995.
XX
PF 12-MAR-1991; 91AU-0074762.
XX
PR 12-MAR-1991; 91AU-0074762.
PR 13-AUG-1993; 93AU-0044664.
XX
PA (PEPT-) PEPTIDE TECHNOLOGY LTD.
XX
PI Ferrante A, Rathjen DA, Widmer F;
XX
DR WPI; 1995-115742/16.
XX
PT Novel peptides which stimulate neutrophils - are fragments of
PT tumour necrosis factor
XX
PS Disclosure; Page 15; 51pp; English.
XX
CC New peptides are provided which prime neutrophils for superoxide
CC production and an enhanced respiratory burst following treatment
CC with N-formyl-L-methionine-L-leucyl-L-phenylalanine. The peptides are
CC described generically. They are fragments from the region of amino acids
CC 54 to 94 of human TNF, or analogues of such fragments. Their
CC neutrophil-stimulating activity can be used in the treatment of diseases
CC such as AIDS, cancer, rheumatoid arthritis, ARDS, cystic fibrosis,
CC tuberculosis, Crohn's disease, sarcoidosis, leprosy, syphilis and
CC malaria. The present sequence is one of 6 specific peptides having the
CC above activity and which fit the generic formula.
XX
SQ Sequence 22 AA;
Query Match 34.8%; Score 40; DB 16; Length 22;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YQTKVNLL 8
Db 15 YQTKVNLL 22
RESULT 8
AAR06772
ID AAR06772 standard; protein; 14 AA.
XX
AC AAR06772;
XX
DT 23-OCT-1990 (first entry)
XX
DE Tumour necrosis factor derived peptide.
XX
KW Tumour necrosis factor; TNF; neoplastic disease; autoimmune
KW disease; infection; inflammation; transplant rejection; cyclic.
XX
OS Synthetic.
XX
PN DE3841759-A.
XX
PD 13-JUN-1990.
XX
PF 12-DEC-1988; 88DE-3841759.
XX

```

PR 12-DEC-1988; 88DE-38411759.
XX (BADI) BASF AG.
XX Bohm HJ, Daum L, Haupt A, Schmied B, Walker N, Zechel JC;
XX WPI; 1990-186576/25.
XX
XX New tumour necrosis factor derived peptides- for treating or preventing
PT neoplastic and autoimmune diseases, infection, inflammation and
PT transplant rejection.
XX
XX Example 40; Page 13; 16pp; German.
XX
XX This peptide is an example of a highly generic sequence of the
CC formula X-A-Y.
CC A= QRETPEGAERK, HRETPEWAEAKP, HRETPEAEAPMA, PROTPEGAELKP, PGLQEP,
CC PGQGP or PGLQGP;
CC X= G-NH-CHM-CO, G-NH-CHM-CO-W, G-R-NH-CHM-CO or G-R-NH-CHM-CO-W;
CC Y= Z, NH-CHQ-COZ, V-NH-CHQ-COZ, NH-CHQ-CO-U-Z or V-NH-CHQ-CO-U-Z;
CC G= H or an amino protecting group;
CC Z= OH, NH2 or carboxy protecting group; or G and Z together are a
CC covalent bond or the gp. CO(CH2)2aNH; a-1-12;
CC R, U, V and W= peptide chains of 1-4 naturally occurring alpha aminoacids;
CC M and Q= H, isopropyl, CHMe.Et, phenyl, CH(OH), 3-indolyl- or
CC 4-imidazolyl-methyl or (CH2)bt; b-1-6;
CC T= OH, MeO, MeS, isopropyl, phenyl (opt. 4-OH, substd.), HS, NH2, COOH,
CC CONH2, or NH2 C (NH) NH; or
CC M and Q together are (CH2)c-S-(CH2)d, (CH2)eCO NH-(CH2)f or
CC (CH)2eNH CO(CH2)gNH CO(CH2) f; c and d-1-4; e and f-1-6; g-1-12.
CC The peptide is a low mol. wt. deriv. of TNF.
CC See also DE3841753-55, DE3841759, DE3841761-64, DE3841767-68.
XX
XX Sequence 14 AA;
SQ
Query Match 33.0%; Score 38; DB 11; Length 14;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 16 QRETPEG 22
Db | | | | | | |
2 QRETPEG 8
RESULT 9
AAY82194
ID AAY82194 standard; peptide; 14 AA.
XX
XX AAY82194;
XX
XX 08-JUN-2000 (first entry)
XX
XX Tumour necrosis factor alpha derived peptide #1.
XX
XX Tumour necrosis factor alpha; TNF-alpha; human; mouse; oedema;
KW proinflammatory; pulmonary oedema.
XX
XX Homo sapiens.
XX
XX WO200009149-A1.
XX
XX 24-FEB-2000.
XX
XX 10-AUG-1999; 99WO-EP05806.
XX
XX 14-AUG-1998; 98EP-0870180.
PR 18-SEP-1998; 98EP-0870198.
PR 21-OCT-1998; 98EP-0870222.
XX
XX (INNO-) INNOGENETICS NV.
XX
XX Lucas R, De Baetselier P, Pugin J, Bloc A, Fransen L;
PI
XX

DR WPI; 2000-282855/24.
XX
XX Use of peptides derived from human or mouse tissue necrosis
PT factor-alpha (TNF-alpha), and comprising 7-17 contiguous amino acids,
PT for preventing or treating oedema -
XX
XX Claim 5; Page 16; 26pp; English.
XX
XX The present invention describes the use of peptides comprising a chain
CC of 7-17 contiguous amino acids derived from the Ser100-Glu116 region
CC of human tumour necrosis factor-alpha (TNF-alpha), or Ser99-Glu115
CC region of mouse TNF-alpha, for treating oedema. The peptides form
CC pharmaceutical compositions for treating oedema, especially pulmonary
CC oedema. The peptides are non-toxic, whilst retaining the oedema
CC resorption-inducing capacity as TNF. The present sequence represents
CC a specifically claimed TNF-alpha peptide from the present invention.
XX
XX Sequence 14 AA;
SQ
Query Match 33.0%; Score 38; DB 21; Length 14;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 16 QRETPEG 22
Db | | | | | | |
1 QRETPEG 7
RESULT 10
AAR60233
ID AAR60233 standard; peptide; 17 AA.
XX
XX AAR60233;
XX
XX 16-MAR-1995 (first entry)
DT hTNF-alpha tip.
XX
XX TNF-alpha: tumor necrosis factor-alpha; tip peptide; mutein; cancer;
KW sepsis; inflammation; cytokine; metastasis; lectin; adhesion;
KW mutagenesis; trypanoside.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Misc-difference 1 /note= "N-terminal biotin Gly-Gly"
FT
XX
XX WO9418325-A.
XX
XX 18-AUG-1994.
XX
XX 02-FEB-1994; 94WO-EP00286.
XX
XX 03-FEB-1993; 93EP-0400262.
XX
XX (INNO-) INNOGENETICS NV SA.
XX
XX De Baetselier P, Fransen L, Lucas R, Sablon E;
PI
XX WPI; 1994-279746/34.
XX
XX New tumour necrosis factor -alpha muteins, antibodies and
PT antisense peptide(s) - used in the treatment of diseases and
PT conditions associated with the in vivo activities of TNF-A eg
PT cancer, sepsis, inflammation, etc
XX
XX Disclosure; Page 61; 132pp; English.
XX
XX The TNF-alpha tip peptides given in AAR60232-42 were modified with
CC N-terminal biotin-Gly-Gly moieties and were used to demonstrate
CC that the tip region of mouse and human TNF-alpha contains the
CC trypanosomal and lectin-like activities of the molecule and is

CC is involved in TNF-induced lethal shock.

XX Sequence 17 AA;

Query Match 33.0%; Score 38; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 QRETPEG 22

Db 3 QRETPEG 9

RESULT 11

AA82196
ID AAY82196 standard; peptide; 17 AA.

XX AAY82196;

AC AAY82196;

DT 08-JUN-2000 (first entry)

DE Tumour necrosis factor alpha derived circularised peptide #1.

KW Tumour necrosis factor alpha; TNF-alpha; human; mouse; oedema;

KW proinflammatory; pulmonary oedema; cyclic.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Disulfide-bond 1..17

XX WO200009149-A1.

PD 24-FEB-2000.

XX 10-AUG-1999; 99WO-EP05806.

XX 14-AUG-1998; 98EP-0870180.

PR 18-SEP-1998; 98EP-0870198.

PR 21-OCT-1998; 98EP-0870222.

XX (INNO-) INNOGENETICS NV.

PI Lucas R, De Baetselier P, Pugin J, Bloc A, Fransen L;

XX WPI; 2000-282855/24.

PT Use of peptides derived from human or mouse tissue necrosis
factor-alpha (TNF-alpha), and comprising 7-17 contiguous amino acids,
PT for preventing or treating oedema -

XX Claim 8; Page 16; 26pp; English.

XX The present invention describes the use of peptides comprising a chain
of 7-17 contiguous amino acids derived from the Ser100-Glu116 region
of human tumour necrosis factor-alpha (TNF-alpha), or Ser99-Glu115
region of mouse TNF-alpha, for treating oedema. The peptides form
CC pharmaceutical compositions for treating oedema, especially pulmonary
CC oedema. The peptides are non-toxic, whilst retaining the oedema
CC resorption-inducing capacity as TNF. The present sequence represents
CC a specifically claimed TNF-alpha circularised peptide from the present
CC invention.

XX Sequence 17 AA;

Query Match 33.0%; Score 38; DB 21; Length 17;

Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 QRETPEG 22

Db 3 QRETPEG 9

RESULT 12

AAG64014

ID AAG64014 standard; Peptide; 15 AA.

XX AAG64014;

AC AAG64014;

DT 06-SEP-2001 (first entry)

DE Human cytochrome C domain-containing TNFR/NGFR protein 51 N-terminus.

XX Human; cytochrome c domain; tumour necrosis factor receptor; TNFR;

KW nerve growth factor receptor; NGFR; TNFR/NGFR protein 51; cancer;

KW haemopathy; human immunodeficiency virus; HIV; infection;

KW immunological disease; inflammation; antiinflammatory; cytostatic;

KW immunomodulatory; haemostatic.

XX Homo sapiens.

XX WO200140296-A1.

XX 07-JUN-2001.

XX 27-NOV-2000; 2000WO-CN00506.

XX 29-NOV-1999; 99CN-0124139.

XX (BIOR-) BIOROAD GENE DEV LTD SHANGHAI.

XX Mao Y, Xie Y;

XX WPI; 2001-374791/39.

XX Human cytochrome c domain-containing TNFR/NGFR protein 51 and encoded
polynucleotide, applicable in diagnosis and treatment of malignant
PT tumor, hemopathy, HIV infection, immunological diseases and various
PT inflammations -

XX Example 5; Page 14; 37pp; Chinese.

XX The invention relates to an isolated polypeptide of human cytochrome c
domain-containing tumour necrosis factor receptor/nerve growth factor
CC receptor (TNFR/NGFR) protein 51. The polypeptide comprises a sequence
CC of 461 amino acids, or its fragment, analogue or derivative. The
CC polypeptide and the polynucleotide encoding it are useful in the
CC diagnosis and treatment of malignant tumours, haemopathy, HIV infection,
CC immunological diseases and inflammation. The present sequence
CC is the N-terminus of the polypeptide of the invention.

XX Sequence 15 AA;

Query Match 32.2%; Score 37; DB 22; Length 15;

Best Local Similarity 50.0%; Pred. No. 26;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 8 LSAIKSPQCR 17

Db 1 MNAVQKPCR 10

RESULT 13

ABB33440

ID ABB33440 standard; Peptide; 17 AA.

XX ABB33440;

DT 04-FEB-2002 (first entry)

DE Peptide #946 encoded by human foetal liver single exon probe.

XX Human; foetal liver; gene expression; single exon nucleic acid probe.

XX Homo sapiens.

XX WO200157277-A2.
PN
XX
XX
PD
XX
XX
PF 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US00669.
XX
XX 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI
XX WPI; 2001-483447/52.
XX
XX Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human fetal liver -
XX
XX Claim 27; SEQ ID NO 26075; 639pp + sequence listing; English.
XX
XX The invention relates to a single exon nucleic acid probe for
CC measuring human gene expression in a sample derived from human foetal
CC liver. The single exon nucleic acid probes may be used for predicting,
CC measuring and displaying gene expression in samples derived from human
CC foetal liver. The present sequence is a peptide encoded by a single exon
CC nucleic acid probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 17 AA;
SQ
Query Match 31.3%; Score 36; DB 22; Length 17;
Best Local Similarity 66.7%; Pred. No. 44;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 12 KSPCQRETP 20
Db :||| |||
9 QSPCGREAP 17
RESULT 14
ABB18899
ID ABB18899 standard; Protein; 17 AA.
XX
XX AC ABB18899;
XX
XX 23-JAN-2002 (first entry)
DT
DE Protein #898 encoded by probe for measuring heart cell gene expression.
XX
XX Human; gene expression; heart; microarray; vascular system;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease.
XX
XX Homo sapiens.
OS
XX WO200157274-A2.
PN
XX 09-AUG-2001.
PD
XX 30-JAN-2001; 2001WO-US00666.
XX
XX 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI
XX WPI; 2001-488899/53.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
PT hearts -
XX
XX Claim 15; SEQ ID NO 20669; 530pp; English.
XX
XX The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart (see
CC ABA21535-ABA41305). The present sequence is a protein encoded by one such
CC probe. The probes may be used for predicting, measuring and displaying
CC gene expression in samples derived from the human heart via microarrays.
CC By measuring gene expression, the probes are useful for predicting,
CC diagnosing, grading, staging, monitoring and prognosing diseases of the
CC human heart and vascular system e.g. cardiovascular disease,
CC hypertension, cardiac arrhythmias and congenital heart disease.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 17 AA;
SQ
Query Match 31.3%; Score 36; DB 22; Length 17;
Best Local Similarity 66.7%; Pred. No. 44;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 12 KSPCQRETP 20
Db :||| |||
9 QSPCGREAP 17
RESULT 15
AAM54225
ID AAM54225 standard; Protein; 17 AA.
XX
XX AC AAM54225;
XX
XX 05-NOV-2001 (first entry)
DT
XX
XX Human brain expressed single exon probe encoded protein SEQ ID NO: 26330.
DE
XX Human; brain expressed exon; gene expression analysis; probe;
KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW epilepsy; cancer.
XX
XX Homo sapiens.
OS
XX WO200157275-A2.
PN
XX 09-AUG-2001.
PD
XX 30-JAN-2001; 2001WO-US00667.
XX
XX 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI
XX

DR WPI; 2001-483446/52.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT brains -
XX
XX
PS Example 4; SEQ ID NO: 26330; 650pp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is a protein encoded by one of
XX the probes of the invention.
XX
SQ Sequence 17 AA;

Query Match 31.3%; Score 36; DB 22; Length 17;
Best Local Similarity 66.7%; Pred. No. 44;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 12 KSPCORETP 20
:||| |||
Db 9 QSPCGREAP 17

Search completed: December 4, 2002, 13:36:31
Job time : 37 secs

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OM protein - protein search, using sw model

Run on: December 4, 2002, 13:37:30 ; Search time 11 Seconds
(without alignments)
32.485 Million cell updates/sec

Title: US-09-754-004-2

Perfect score: 115

Sequence: 1 YQKVNLSAISKPCQRETPG 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 103943 seqs, 16242309 residues

Total number of hits satisfying chosen parameters: 33790

Minimum DB seq length: 0

Maximum DB seq length: 22

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	115	100.0	22	8	US-08-602-272-2
2	115	100.0	22	10	US-09-754-004-2
3	36	31.3	17	10	US-09-864-761-34197
4	33	28.7	19	10	US-09-864-761-35911
5	31	27.0	15	10	US-09-865-644-2
6	31	27.0	21	10	US-09-864-761-35348
7	29	25.2	12	10	US-09-791-378-27
8	29	25.2	18	10	US-09-746-742-40
9	29	25.2	20	10	US-09-864-761-48431
10	29	25.2	20	10	US-09-746-742-48
11	28	24.3	16	10	US-09-107-058-10
12	28	24.3	18	10	US-09-864-761-38964
13	27	23.5	19	12	US-10-012-030A-78
14	27	23.5	21	9	US-10-038-612-42
15	27	23.5	21	9	US-09-187-693-73
16	27	23.5	21	10	US-09-864-761-41730
17	27	23.5	21	10	US-09-864-761-44194
18	27	23.5	22	9	US-10-038-612-150
19	26	22.6	16	10	US-09-879-957-163

Sequence 8, Appli
Sequence 19, Appli
Sequence 48162, A
Sequence 47162, A
Sequence 15, Appli
Sequence 16, Appli
Sequence 62, Appli
Sequence 15, Appli
Sequence 16, Appli
Sequence 15, Appli
Sequence 16, Appli
Sequence 161, Appl
Sequence 33971, A
Sequence 41239, A
Sequence 185, App
Sequence 73, Appli
Sequence 12, Appli
Sequence 7, Appli
Sequence 208, App
Sequence 63, Appli
Sequence 6, Appli
Sequence 61, Appli
Sequence 35, Appli
Sequence 5, Appli
Sequence 479, App
Sequence 36, Appli

ALIGNMENTS

RESULT 1
US-08-602-272-2
; Sequence 2, Application US/08602272
; Patent No. US20020081306A1
; GENERAL INFORMATION:
; APPLICANT: Elliott, Michael J.
; APPLICANT: Maini, Ravinder N.
; APPLICANT: Feldmann, Marc
; TITLE OF INVENTION: Methods of Preventing or Treating
; TITLE OF INVENTION: Cardiovascular, Cerebrovascular and Thrombotic Disorders
; TITLE OF INVENTION: with Tumor Necrosis Factor Antagonists
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173-4799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,272
; FILING DATE:
; CLASSIFICATION: 504
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: KIR96-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-602-272-2

Query Match 100.0%; Score 115; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.9e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YQTKVNLSSAIKSPQORETPEG 22
|||||
DB 1 YQTKVNLSSAIKSPQORETPEG 22

RESULT 2

US-09-754-004-2
; Sequence 2, Application US/09754004
; Patent No. US20020010180A1
; GENERAL INFORMATION:
; APPLICANT: Marc Feldmann
; TITLE OF INVENTION: TNF Alpha Antagonists and Methotrexate
; TITLE OF INVENTION: in the Treatment of TNF-Mediated Disease
; FILE REFERENCE: 2891.1001-026
; CURRENT APPLICATION NUMBER: US/09/754,004
; CURRENT FILING DATE: 2001-01-03
; PRIOR APPLICATION NUMBER: 08/690,775
; PRIOR FILING DATE: 1996-08-01
; PRIOR APPLICATION NUMBER: 08/607,419
; PRIOR FILING DATE: 1996-02-28
; PRIOR APPLICATION NUMBER: PCT/GB94/00462
; PRIOR FILING DATE: 1994-03-10
; PRIOR APPLICATION NUMBER: PCT/GB93/02070
; PRIOR FILING DATE: 1993-10-06
; PRIOR APPLICATION NUMBER: 07/958,248
; PRIOR FILING DATE: 1992-10-08
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-754-004-2

Query Match 100.0%; Score 115; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.9e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YQTKVNLSSAIKSPQORETPEG 22
|||||
DB 1 YQTKVNLSSAIKSPQORETPEG 22

RESULT 3

US-09-864-761-34197
; Sequence 34197, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecomica-x-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 34197
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL049844.6
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.84
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.8
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
; OTHER INFORMATION: EST_HUMAN HIT: AUI36661.1, EVALUE 9.00e-04
US-09-864-761-34197

Query Match 31.3%; Score 36; DB 10; Length 17;
Best Local Similarity 66.7%; Pred. No. 6.5;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 12 KSPCORETP 20
:|||||
DB 9 QSPCGREAP 17

RESULT 4

US-09-864-761-35911
; Sequence 35911, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Aecomica-x-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456

;
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 35911
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AP000356.1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.99
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.5
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 8.5
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.4
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.9
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 9.3
; OTHER INFORMATION: EST_HUMAN HIT: H19181.1, EVALUATE 5.00e-05
US-09-864-761-35911

Query Match 28.7%; Score 33; DB 10; Length 19;
Best Local Similarity 50.0%; Pred. No. 22;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 13 SPCORETPEG 22
Db 8 TPCRRSSEG 17

RESULT 5
US-09-865-644-2
; Sequence 2, Application US/09865644
; Patent No. US20020045188A1
; GENERAL INFORMATION:
; APPLICANT: Kamb et al
; TITLE OF INVENTION: METHODS FOR VALIDATING POLYPEPTIDE TARGETS THAT CORRELATE TO CELLULAR PHENOTYPES
; FILE REFERENCE: 29345/37561
; CURRENT APPLICATION NUMBER: US/09/865,644
; CURRENT FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 24

;
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Peptide Binder of HPV E6
US-09-865-644-2

Query Match 27.0%; Score 31; DB 10; Length 15;
Best Local Similarity 46.2%; Pred. No. 35;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 YQTKVNLSAISK 13
Db 3 YSTAMNLLDSLLS 15

RESULT 6

US-09-864-761-35348
; Sequence 35348, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 35348
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:

; OTHER INFORMATION: MAP TO AC008116.8
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.4
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.6
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.2
; OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.4
; OTHER INFORMATION: EST_HUMAN HIT: BE697125.1, EVALU6 1.00e-05
US-09-864-761-35348

Query Match 27.0%; Score 31; DB 10; Length 21;
Best Local Similarity 71.4%; Pred. No. 52;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 13 SPCQRET 19
:|||||
Db 11 APCQRAT 17

RESULT 7
US-09-791-378-27
; Sequence 27, Application US/09791378
; Patent No. US20020142303A1
; GENERAL INFORMATION:
; APPLICANT: Parekh, Rajesh
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF
; FILE REFERENCE: 9195-061-999
; CURRENT APPLICATION NUMBER: US/09791,378
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/750,395
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 677
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-378-27

Query Match 25.2%; Score 29; DB 10; Length 12;
Best Local Similarity 44.4%; Pred. No. 57;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 11 IKSPCQRET 19
:|||||
Db 2 VTDPQCADT 10

RESULT 8
US-09-746-742-40
; Sequence 40, Application US/09746742
; Patent No. US20020077284A1
; GENERAL INFORMATION:
; APPLICANT: Eckert, Deborah M.
; APPLICANT: Chan, David C.
; APPLICANT: Malashkevich, Vladimir
; APPLICANT: Carr, Peter A.
; APPLICANT: Kim, Peter S.
; TITLE OF INVENTION: Inhibitors of HIV Membrane Fusion
; CURRENT APPLICATION NUMBER: US/09746,742
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: PCT/US99/17351
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: US 60/043,280
; PRIOR FILING DATE: 1997-04-17
; PRIOR APPLICATION NUMBER: US 09/062,241
; PRIOR FILING DATE: 1998-04-17

; PRIOR APPLICATION NUMBER: US 60/094,676
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: US 60/100,265
; PRIOR FILING DATE: 1998-09-14
; PRIOR APPLICATION NUMBER: US 60/101,058
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: US 60/132,295
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D-peptide
US-09-746-742-40

Query Match 25.2%; Score 29; DB 10; Length 18;
Best Local Similarity 50.0%; Pred. No. 91;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 12 KSPCQRETPE 21
| | | | |
Db 2 KGACRSRQPE 11

RESULT 9
US-09-864-761-48431
; Sequence 48431, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aesomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263..6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21

;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 48431
;; LENGTH: 20
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO L78810.1
;; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.91
;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1
;; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 0.94
;; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1
;; OTHER INFORMATION: EST_HUMAN HIT: BE827799.1, EVALUATE 2.00e-05
US-09-864-761-48431

Query Match 25.2%; Score 29; DB 10; Length 20;
Best Local Similarity 55.6%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 14 PCQRETPEG 22
||| : ||
Db 3 PCQMDYGE 11

RESULT 10
US-09-746-742-48
;; Sequence 48, Application US/09746742
;; Patent No. US20020077284A1
;; GENERAL INFORMATION:
;; APPLICANT: Eckert, Deborah M.
;; APPLICANT: Chan, David C.
;; APPLICANT: Malashkevich, Vladimir
;; APPLICANT: Carr, Peter A.
;; APPLICANT: Kim, Peter S.
;; TITLE OF INVENTION: Inhibitors of HIV Membrane Fusion
;; FILE REFERENCE: 0399.1192-008
;; CURRENT APPLICATION NUMBER: US/09/746,742
;; CURRENT FILING DATE: 2000-12-21
;; PRIOR APPLICATION NUMBER: PCT/US99/17351
;; PRIOR FILING DATE: 1999-07-30
;; PRIOR APPLICATION NUMBER: US 60/043,280
;; PRIOR FILING DATE: 1997-04-17
;; PRIOR APPLICATION NUMBER: US 09/062,241
;; PRIOR FILING DATE: 1998-04-17
;; PRIOR APPLICATION NUMBER: US 60/094,676
;; PRIOR FILING DATE: 1998-07-30
;; PRIOR APPLICATION NUMBER: US 60/100,265
;; PRIOR FILING DATE: 1998-09-14
;; PRIOR APPLICATION NUMBER: US 60/101,058
;; PRIOR FILING DATE: 1998-09-18
;; PRIOR APPLICATION NUMBER: US 60/132,295
;; PRIOR FILING DATE: 1999-05-03
;; NUMBER OF SEQ ID NOS: 68
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 48
;; LENGTH: 20
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: D-peptide
US-09-746-742-48

Query Match 25.2%; Score 29; DB 10; Length 20;
Best Local Similarity 50.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 12 KSPCORETPE 21
.: | | | | |
Db 4 KGACSRSQPE 13

RESULT 11
US-09-107-058-10
;; Sequence 10, Application US/09107058
;; Patent No. US20010010922A1
;; GENERAL INFORMATION:
;; APPLICANT: Dalla-Favera, Riccardo
;; APPLICANT: Niu, Hui-Feng
;; TITLE OF INVENTION: CLONING AND USES OF THE GENETIC
;; TITLE OF INVENTION: LOCUS bcl-6
;; NUMBER OF SEQUENCES: 12
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Cooper & Dunham LLP
;; STREET: 1185 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: United States of America
;; ZIP: 10036
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/107,058
;; FILING DATE:
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: White, John P.
;; REGISTRATION NUMBER: 28,678
;; REFERENCE/DOCKET NUMBER: 0575/43771-A-PCT-US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 278-0400
;; TELEFAX: (212) 391-0525
;; TELEX: 422523 COOP UI
;; INFORMATION FOR SEQ ID NO: 10:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 16 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-09-107-058-10

Query Match 24.3%; Score 28; DB 10; Length 15;
Best Local Similarity 55.6%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 12 KSPCORETP 20
| | | | |
Db 1 KSDCQPNSP 9

RESULT 12
US-09-864-761-38964
;; Sequence 38964, Application US/09864761
;; Patent No. US20020048763A1
;; GENERAL INFORMATION:
;; APPLICANT: Penn, Sharron G.
;; APPLICANT: Rank, David R.
;; APPLICANT: Hanzel, David K.
;; APPLICANT: Chen, Wensheng
;; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;; FILE REFERENCE: Aecmica-X-1
;; CURRENT APPLICATION NUMBER: US/09/864,761
;; CURRENT FILING DATE: 2001-05-23
;; PRIOR APPLICATION NUMBER: US 60/180,312
;; PRIOR FILING DATE: 2000-02-04
;; PRIOR APPLICATION NUMBER: US 60/207,456
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: US 09/632,366

; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 38964
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC002099.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.6
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.6
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.1
US-09-864-761-38964

Query Match 24.3%; Score 28; DB 10; Length 18;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 13 SPCQRTPEG 22
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Db 1 SPCARPGSDG 10

RESULT 13
US-10-012-030A-78
; Sequence 78, Application US/10012030A
; Patent No. US20020151497A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel A.
; TITLE OF INVENTION: TREATMENT OF PROSTATE CANCER BY
; INHIBITING LYN TYROSINE KINASE
; FILE REFERENCE: BEN-SASSON-1B
; CURRENT APPLICATION NUMBER: US/10/012,030A
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: US 09/735,279
; PRIOR FILING DATE: 2000-12-11
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: FastSeq for Windows, Version 4.0

; SEQ ID NO 78
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-012-030A-78

Query Match 23.5%; Score 27; DB 12; Length 19;
Best Local Similarity 46.2%; Pred. No. 2e+02;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 YQTKVNLLSAISK 13
| | :|| :||
Db 4 YMAKGSLLDFLKS 16

RESULT 14
US-10-038-612-42
; Sequence 42, Application US/10038612
; Patent No. US20020160478A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel A.
; TITLE OF INVENTION: Short Peptides Which Selectively
; Modulate the Activity of Protein Kinases
; FILE REFERENCE: 1242.1029-000 (CMCC-679)
; CURRENT APPLICATION NUMBER: US/10/038,612
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 09/161,094
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 21
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: Lyn
US-10-038-612-42

Query Match 23.5%; Score 27; DB 9; Length 21;
Best Local Similarity 46.2%; Pred. No. 2.3e+02;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 YQTKVNLLSAISK 13
| | :|| :||
Db 3 YMAKGSLLDFLKS 15

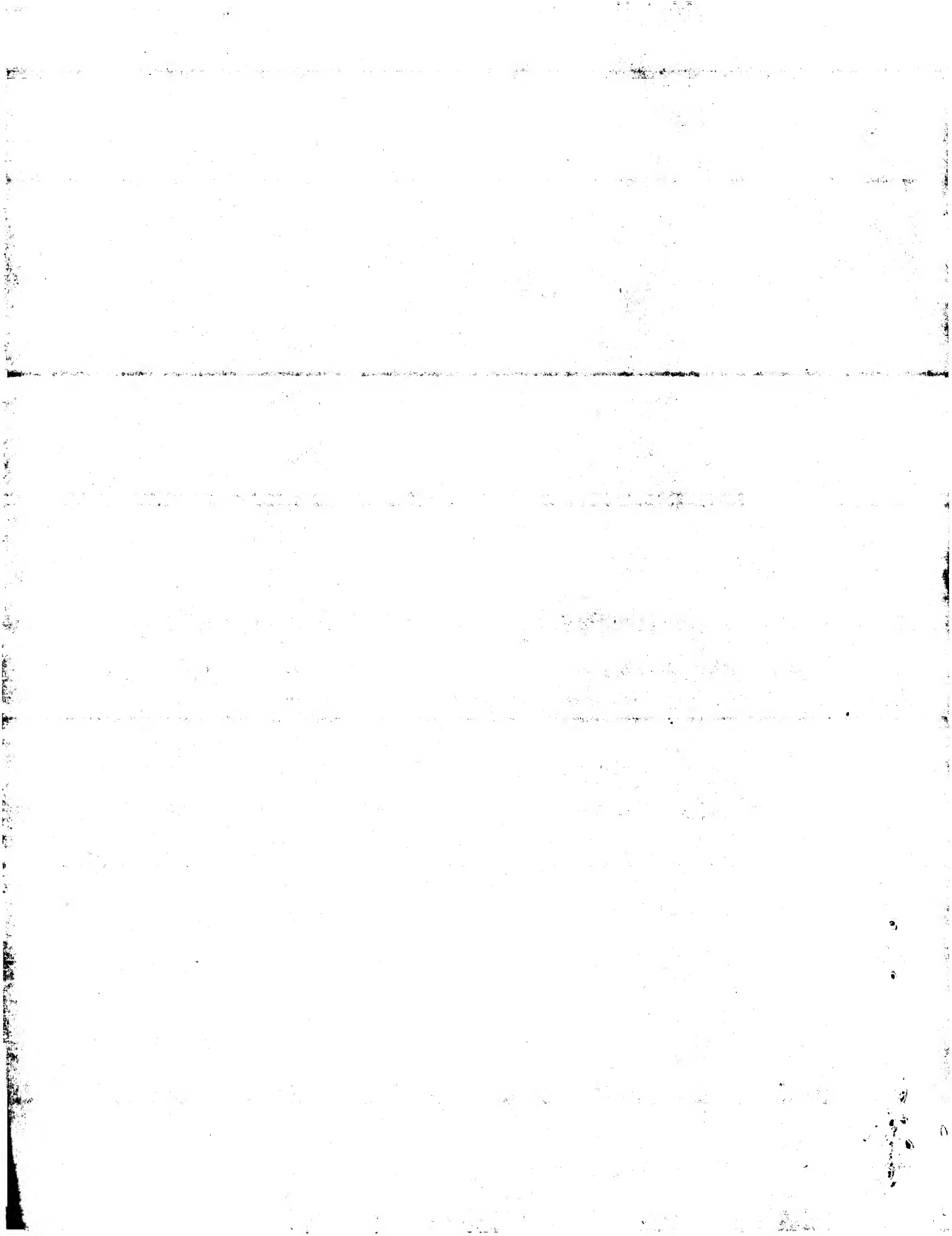
RESULT 15
US-09-187-693-73
; Sequence 73, Application US/09187693
; Patent No. US20020173629A1
; GENERAL INFORMATION:
; APPLICANT: Jakobovits, Aya
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Gallo, Michael
; APPLICANT: Jia, Xiao-Chi
; TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
; Growth Factor Receptor
; FILE REFERENCE: Cell 4.20 CIP2
; CURRENT APPLICATION NUMBER: US/09/187,693
; CURRENT FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 09/162,280
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 08/851,362
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 73
; LENGTH: 21
; TYPE: PRT
; ORGANISM: human

US-09-187-693-73

Query Match 23.5%; Score 27; DB 9; Length 21;
Best Local Similarity 57.1%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 13 SPCQRET 19
: | | |
Db 13 APCSRST 19

Search completed: December 4, 2002, 13:41:06
Job time : 12 secs



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OM protein - protein search, using sw model

Run on: December 4, 2002, 13:35:55 ; Search time 14 Seconds
(without alignments)
46.236 Million cell updates/sec

Title: US-09-754-004-2

Perfect score: 115

Sequence: 1 YQTKVLLSAIKSPQRETPEG 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 140335

Minimum DB seq length: 0

Maximum DB seq length: 22

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	115	100.0	22	4	US-08-690-775-2
2	79	68.7	16	1	US-08-107-235-5
3	79	68.7	16	3	US-08-714-960B-5
4	79	68.7	16	4	US-09-598-784-5
5	67	58.3	16	1	US-08-178-268-39
6	41	35.7	14	3	US-08-377-781A-10
7	40	34.8	11	1	US-08-107-235-16
8	40	34.8	11	3	US-08-714-960B-16
9	40	34.8	11	4	US-09-598-784-16
10	40	34.8	14	1	US-08-107-235-14
11	40	34.8	14	3	US-08-714-960B-14
12	40	34.8	14	4	US-09-598-784-14
13	40	34.8	22	1	US-08-107-235-11
14	40	34.8	22	1	US-08-178-268-45
15	40	34.8	22	3	US-08-714-960B-11
16	40	34.8	22	4	US-09-598-784-11
17	38	33.0	17	2	US-08-500-860A-25
18	34	29.6	15	1	US-08-318-200-6
19	34	29.6	15	3	US-08-414-174-6
20	34	29.6	15	4	US-09-009-953-176
21	34	29.6	15	4	US-09-009-953-183
22	33	28.7	11	2	US-08-824-405-19
23	33	28.7	14	2	US-08-824-405-20
24	33	28.7	22	4	US-08-906-156A-76
25	32	27.8	20	2	US-07-894-063A-10
26	32	27.8	21	2	US-08-934-915-16
27	31	27.0	18	1	US-08-575-863-10

28	31	27.0	18	1	US-08-815-530-10	Sequence 10, Appl
29	31	27.0	22	1	US-08-262-037-97	Sequence 97, Appl
30	30	26.1	22	4	US-08-851-089-7	Sequence 7, Appl
31	29.5	25.7	20	3	US-08-256-747C-13	Sequence 13, Appl
32	29.5	25.7	20	4	US-08-834-130A-13	Sequence 13, Appl
33	29	25.2	8	6	5164481-11	Patent No. 5164481
34	29	25.2	15	2	US-08-637-759B-239	Sequence 239, App
35	29	25.2	15	2	US-08-455-079-5	Sequence 5, Appl
36	29	25.2	15	3	US-08-871-355A-239	Sequence 239, App
37	29	25.2	15	4	US-09-201-945-239	Sequence 239, App
38	29	25.2	19	6	5164481-3	Patent No. 5164481
39	29	25.2	20	1	US-08-103-742-34	Sequence 34, Appl
40	29	25.2	22	1	US-08-193-521-11	Sequence 11, Appl
41	29	25.2	22	1	US-08-434-120-105	Sequence 105, App
42	29	25.2	22	1	US-08-465-325-104	Sequence 104, App
43	29	25.2	22	2	US-08-455-079-18	Sequence 18, Appl
44	29	25.2	22	4	US-09-115-737-104	Sequence 104, App
45	28	24.3	10	4	US-08-836-075A-190	Sequence 190, App

ALIGNMENTS

RESULT 1
US-08-690-775-2
; Sequence 2, Application US/08690775
; Patent No. 6270766
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Marc
; TITLE OF INVENTION: ANTI-TNF ANTIBODIES AND METHOTREXATE IN
; TITLE OF INVENTION: THE TREATMENT OF AUTOIMMUNE DISEASE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: TWO MILITIA DRIVE
; CITY: LEXINGTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/690,775
; FILING DATE: 01-AUG-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/607,419
; FILING DATE: 28-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB94/00462
; FILING DATE: 15-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/02070
; FILING DATE: 06-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/958,248
; FILING DATE: 08-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook Esq., David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: KIR92-01A4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS:

; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-690-775-2

Query Match 100.0%; Score 115; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 6.8e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YQTKVNLISAISPCQRETPPEG 22
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DB 1 YQTKVNLISAISPCQRETPPEG 22

RESULT 2

US-08-107-235-5
; Sequence 5, Application US/08107235
; Patent No. 5587457

; GENERAL INFORMATION:

; APPLICANT: Rathjen, Deborah A

; APPLICANT: Ferrante, Antonio

; APPLICANT: Widmer, Fred

; TITLE OF INVENTION: Neutrophil Stimulating Peptides

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Allegretti & Witcoff, Ltd.

; STREET: 10 S. Wacker Dr.

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/107,235

; FILING DATE: 16-AUG-1993

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/930,415

; FILING DATE: 12-MAR-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: McDonnell, John J

; REGISTRATION NUMBER: 26,949

; REFERENCE/DOCKET NUMBER: 92,622A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312-715-1000

; TELEFAX: 312-715-1234

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 16 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FEATURE:

; NAME/KEY: Peptide

; LOCATION: 1..16

; OTHER INFORMATION: /note= "PEPTIDE 303 (94-109)"

US-08-107-235-5

Query Match 68.7%; Score 79; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LSAIKSPCQRETPPEG 22

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DB 1 LSAIKSPCQRETPPEG 15

RESULT 3

US-08-714-960B-5

; Sequence 5, Application US/08714960B

; Patent No. 6121237
; GENERAL INFORMATION:
; APPLICANT: RATHJEN, Deborah A
; APPLICANT: FERRANTE, Antonio
; TITLE OF INVENTION: Neutrophil Stimulating Peptides
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER & WITCOFF, LTD.
; STREET: 10 S. Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 Mb storage diskette, 3.50 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: IBM compatible PC/MS-DOS
; SOFTWARE: WordPerfect version 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/714,960B
; FILING DATE: 17-SEP-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PJ9065
; FILING DATE: 12-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU91/00086
; FILING DATE: 12-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,415
; FILING DATE: 09-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/107,235
; FILING DATE: 16-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Resis, Robert H.
; REGISTRATION NUMBER: 32,168
; REFERENCE/DOCKET NUMBER: 92,622-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 715-1000
; TELEFAX: (312) 715-1234
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..16
; OTHER INFORMATION: /note= "PEPTIDE 303 (94-109)"
US-08-714-960B-5
Query Match 68.7%; Score 79; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 LSAIKSPCQRETPPEG 22
|||||
DB 1 LSAIKSPCQRETPPEG 15
RESULT 4
US-09-598-784-5
; Sequence 5, Application US/09598784
; Patent No. 6375928
; GENERAL INFORMATION:
; APPLICANT: RATHJEN, Deborah A
; APPLICANT: FERRANTE, Antonio
; TITLE OF INVENTION: Neutrophil Stimulating Peptides
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:

ADDRESSEE: BANNER & WITCOFF, LTD.
STREET: 10 S. Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 mb storage diskette, 3.50 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: IBM compatible PC/MS-DOS
SOFTWARE: WordPerfect version 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/598,784
FILING DATE: 21-Jun-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PJ9065
FILING DATE: 12-MAR-1990
APPLICATION NUMBER: PCT/A091/00086
FILING DATE: 12-MAR-1991
APPLICATION NUMBER: US 07/930,415
FILING DATE: 09-NOV-1992
APPLICATION NUMBER: US 08/107,235
FILING DATE: 16-AUG-1993
APPLICATION NUMBER: US 08/714,960
FILING DATE: 17-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Resis, Robert H.
REGISTRATION NUMBER: 32,168
REFERENCE/DOCKET NUMBER: 11341.00001
TELEPHONE: (312) 715-1000
TELEFAX: (312) 715-1234
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..16
OTHER INFORMATION: /note= "PEPTIDE 303 (94-109)"
US-09-598-784-5
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
Query Match 68.7%; Score 79; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 LSAIKSPCQRETPEG 22
Db 1 LSAIKSPCQRETPEG 15
RESULT 5
US-08-178-268-39
Sequence 39, Application US/08178268
Patent No. 5795859
GENERAL INFORMATION:
APPLICANT: RATHGEN, Deborah A
APPLICANT: WIDMER, Fred
APPLICANT: GRIGG, Geoffrey W
APPLICANT: MACK, Philip O
TITLE OF INVENTION: Peptide which Abrogates TNF and/or LPS Toxicity
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhye P.C.
STREET: 1100 No. 5795859th Glebe Road, 8th Floor
CITY: Arlington
STATE: Virginia
COUNTRY: USA

ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/178,268
FILING DATE: 05-JAN-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: MITCHARD, Leonard C
REGISTRATION NUMBER: 29,009
REFERENCE/DOCKET NUMBER: 47-45
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: both
MOLECULE TYPE: peptide
US-08-178-268-39
Query Match 58.3%; Score 67; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 5.6e-05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 8 LSAIKSPCQRETPEG 22
Db 1 LSAIKSPCQRETPEG 15
RESULT 6
US-08-377-781A-10
Sequence 10, Application US/08377781A
Patent No. 6107273
GENERAL INFORMATION:
APPLICANT: Jameson, Bradford A.
APPLICANT: No. 6107273, Mariadele
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6107273ris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: United States of America
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/377,781A
FILING DATE: 24-JAN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1441
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:

; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: Both
; MOLECULE TYPE: peptide
US-08-377-781A-10

Query Match 35.7%; Score 41; DB 3; Length 14;
Best Local Similarity 87.5%; Pred. No. 1.1;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 15 CORETPEG 22
| | | | |
Db 1 CPRETEG 8

RESULT 7

US-08-107-235-16
; Sequence 16, Application US/08107235
; Patent No. 5587457

GENERAL INFORMATION:

; APPLICANT: Rathjen, Deborah A
; APPLICANT: Ferrante, Antonio
; APPLICANT: Widmer, Fred
; TITLE OF INVENTION: Neutrophil Stimulating Peptides
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Allegretti & Witcoff, Ltd.
; STREET: 10 S. Wacker Dr.
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/107,235
; FILING DATE: 16-AUG-1993

CLASSIFICATION: 530

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,415
; FILING DATE: 12-MAR-1991

ATTORNEY/AGENT INFORMATION:

; NAME: McDonnell, John J
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 92,622A

TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312-715-1000

; TELEFAX: 312-715-1234

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FEATURE:

; NAME/KEY: Peptide

; LOCATION: 1..11

; OTHER INFORMATION: /note= "PEPTIDE 396 (84-94)"

US-08-107-235-16

Query Match 34.8%; Score 40; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YQTKVNLL 8

| | | | |

Db 4 YQTKVNLL 11

RESULT 8

US-09-598-784-16

; Sequence 16, Application US/09598784

; Patent No. 6375928

; GENERAL INFORMATION:

; APPLICANT: Rathjen, Deborah A

; FERRANTE, Antonio

; TITLE OF INVENTION: Neutrophil Stimulating Peptides

US-08-714-960B-16
; Sequence 16, Application US/08714960B
; Patent No. 6121237

GENERAL INFORMATION:

; APPLICANT: Rathjen, Deborah A

; APPLICANT: Ferrante, Antonio

; TITLE OF INVENTION: Neutrophil Stimulating Peptides

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BANNER & WITCOFF, LTD.

; STREET: 10 S. Wacker Drive, Suite 3000

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606

COMPUTER READABLE FORM:

; MEDIUM TYPE: 1.44 MB storage diskette, 3.50 inch

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: IBM compatible PC/MS-DOS

; SOFTWARE: Wordperfect version 6.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/714,960B

; FILING DATE: 17-SEP-1996

CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: AU PJ9065

; FILING DATE: 12-MAR-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/AU91/00086

; FILING DATE: 12-MAR-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/930,415

; FILING DATE: 09-NOV-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/107,235

; FILING DATE: 16-AUG-1993

ATTORNEY/AGENT INFORMATION:

; NAME: Resis, Robert H.

; REGISTRATION NUMBER: 32,168

; REFERENCE/DOCKET NUMBER: 92,622-B

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (312) 715-1000

; TELEFAX: (312) 715-1234

; INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: not relevant

; MOLECULE TYPE: peptide

; FEATURE:

; NAME/KEY: Peptide

; LOCATION: 1..11

; OTHER INFORMATION: /note= "PEPTIDE 396 (84-94)"

US-08-714-960B-16

Query Match 34.8%; Score 40; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YQTKVNLL 8

| | | | |

Db 4 YQTKVNLL 11

RESULT 9

US-09-598-784-16

; Sequence 16, Application US/09598784

; Patent No. 6375928

; GENERAL INFORMATION:

; APPLICANT: Rathjen, Deborah A

; FERRANTE, Antonio

; TITLE OF INVENTION: Neutrophil Stimulating Peptides

NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER & WITCOFF, LTD.
STREET: 10 S. Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb storage diskette, 3.50 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: IBM compatible PC/MS-DOS
SOFTWARE: WordPerfect version 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/598,784
FILING DATE: 21-Jun-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PJ9065
FILING DATE: 12-MAR-1990
APPLICATION NUMBER: PCT/AU91/00086
FILING DATE: 12-MAR-1991
APPLICATION NUMBER: US 07/930,415
FILING DATE: 09-NOV-1992
APPLICATION NUMBER: US 08/107,235
FILING DATE: 16-AUG-1993
APPLICATION NUMBER: US 08/714,960
FILING DATE: 17-SEP-1996

ATTORNEY/AGENT INFORMATION:
NAME: Resis, Robert H.
REGISTRATION NUMBER: 32,168
REFERENCE/DOCKET NUMBER: 11341.00001
TELEPHONE: (312) 715-1000
TELEFAX: (312) 715-1234

INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
FEATURE:

NAME/KEY: Peptide
LOCATION: 1..11
OTHER INFORMATION: /note= "PEPTIDE 396 (84-94)"

SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-598-784-16

Query Match 34.8%; Score 40; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YQTKVNLL 8
Db 4 YQTKVNLL 11

RESULT 10
US-08-107-235-14
Sequence 14, Application US/08107235
Patent No. 5587457
GENERAL INFORMATION:
APPLICANT: Rathjen, Deborah A
APPLICANT: Ferrante, Antonio
APPLICANT: Widmer, Fred
TITLE OF INVENTION: Neutrophil Stimulating Peptides
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 10 S. Wacker Dr.
CITY: Chicago
STATE: Illinois

COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/107,235
FILING DATE: 16-AUG-1993
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/930,415
FILING DATE: 12-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: McDonnell, John J.
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,622A
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234

INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:

NAME/KEY: Peptide
LOCATION: 1..14
OTHER INFORMATION: /note= "PEPTIDE 394 (81-94)"

US-08-107-235-14

Query Match 34.8%; Score 40; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YQTKVNLL 8
Db 7 YQTKVNLL 14

RESULT 11
US-08-714-960B-14
Sequence 14, Application US/08714960B
Patent No. 6121237
GENERAL INFORMATION:
APPLICANT: Rathjen, Deborah A
APPLICANT: Ferrante, Antonio
TITLE OF INVENTION: Neutrophil Stimulating Peptides
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER & WITCOFF, LTD.
STREET: 10 S. Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb storage diskette, 3.50 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: IBM compatible PC/MS-DOS
SOFTWARE: WordPerfect version 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,960B
FILING DATE: 17-SEP-1996
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PJ9065
FILING DATE: 12-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU91/00086
FILING DATE: 12-MAR-1991

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/930,415
;; FILING DATE: 09-NOV-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/107,235
;; FILING DATE: 16-AUG-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Resis, Robert H.
;; REGISTRATION NUMBER: 32,168
;; REFERENCE/DOCKET NUMBER: 92,622-B
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (312) 715-1000
;; TELEFAX: (312) 715-1234
;; INFORMATION FOR SEQ ID NO: 14:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 14 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: not relevant
;; MOLECULE TYPE: peptide
;; FEATURE:
;; NAME/KEY: Peptide
;; LOCATION: 1..14
;; OTHER INFORMATION: /note= "PEPTIDE 394 (81-94)"
;; US-08-714-960B-14

Query Match 34.8%; Score 40; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YQTKVNL 8
Db 7 YQTKVNL 14

RESULT 12

US-09-598-784-14
; Sequence 14, Application US/09598784
; Patent No. 6375928
; GENERAL INFORMATION:
; APPLICANT: RATHJEN, Deborah A
; FERRANTE, Antonio
; TITLE OF INVENTION: Neutrophil Stimulating Peptides
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER & WITCOFF, LTD.
; STREET: 10 S. Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 Mb storage diskette, 3.50 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: IBM compatible PC/MS-DOS
; SOFTWARE: WordPerfect version 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/598,784
; FILING DATE: 21-Jun-2000
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PJ9065
; FILING DATE: 12-MAR-1990
; APPLICATION NUMBER: PCT/AU91/00086
; FILING DATE: 12-MAR-1991
; APPLICATION NUMBER: US 07/930,415
; FILING DATE: 09-NOV-1992
; APPLICATION NUMBER: US 08/107,235
; FILING DATE: 16-AUG-1993
; APPLICATION NUMBER: US 08/714,960
; FILING DATE: 17-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Resis, Robert H.

;; REGISTRATION NUMBER: 32,168
;; REFERENCE/DOCKET NUMBER: 11341.00001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (312) 715-1000
;; TELEFAX: (312) 715-1234
;; INFORMATION FOR SEQ ID NO: 14:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 14 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: not relevant
;; MOLECULE TYPE: peptide
;; FEATURE:
;; NAME/KEY: Peptide
;; LOCATION: 1..14
;; OTHER INFORMATION: /note= "PEPTIDE 394 (81-94)"
;; US-09-598-784-14

Query Match 34.8%; Score 40; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YQTKVNL 8
Db 7 YQTKVNL 14

RESULT 13

US-08-107-235-11
; Sequence 11, Application US/08107235
; Patent No. 5587457
; GENERAL INFORMATION:
; APPLICANT: Rathjen, Deborah A
; APPLICANT: Ferrante, Antonio
; APPLICANT: Widmer, Fred
; TITLE OF INVENTION: Neutrophil Stimulating Peptides
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff, Ltd.
; STREET: 10 S. Wacker Dr.
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/107,235
; FILING DATE: 16-AUG-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,415
; FILING DATE: 12-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McDonnell, John J.
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 92,622A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..22

OTHER INFORMATION: /note= "PEPTIDE 309 (73-94)"
US-08-107-235-11

Query Match 34.8%; Score 40; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YQTKVNLL 8
| | | | | | | |
Db 15 YQTKVNLL 22

RESULT 14

US-08-178-268-45
; Sequence 45, Application US/08178268

Patent No. 5795859

GENERAL INFORMATION:

APPLICANT: RATHJEN, Deborah A

APPLICANT: WIDMER, Fred

APPLICANT: GRIGG, Geoffrey W

APPLICANT: MACK, Philip O

TITLE OF INVENTION: Peptide which Abrogates TNF and/or LPS Toxicity

NUMBER OF SEQUENCES: 47

CORRESPONDENCE ADDRESS:

ADDRESSEE: Nixon & Vanderhye P.C.

STREET: 1100 No. 5795859th Glebe Road, 8th Floor

CITY: Arlington

STATE: Virginia

COUNTRY: USA

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/178,268

FILING DATE: 05-JAN-1994

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: MITCHARD, Leonard C

REGISTRATION NUMBER: 29,009

REFERENCE/DOCKET NUMBER: 47-45

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4000

TELEFAX: (703) 816-4100

INFORMATION FOR SEQ ID NO: 45:

SEQUENCE CHARACTERISTICS:

LENGTH: 22 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: both

MOLECULE TYPE: peptide

US-08-178-268-45

Query Match 34.8%; Score 40; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YQTKVNLL 8
| | | | | | | |
Db 15 YQTKVNLL 22

RESULT 15

US-08-714-960B-11

; Sequence 11, Application US/08714960B

Patent No. 6121237

GENERAL INFORMATION:

APPLICANT: RATHJEN, Deborah A

APPLICANT: FERRANTE, Antonio

TITLE OF INVENTION: Neutrophil Stimulating Peptides

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER & WITCOFF, LTD.
STREET: 10 S. Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb storage diskette, 3.50 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: IBM compatible PC/MS-DOS
SOFTWARE: WordPerfect version 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,960B
FILING DATE: 17-SEP-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PJ9065
FILING DATE: 12-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU91/00086
FILING DATE: 12-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/930,415
FILING DATE: 09-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/107,235
FILING DATE: 16-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Resis, Robert H.
REGISTRATION NUMBER: 32,168
REFERENCE/DOCKET NUMBER: 92,622-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 715-1000
TELEFAX: (312) 715-1234
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..22
OTHER INFORMATION: /note= "PEPTIDE 309 (73-94)"
US-08-714-960B-11

Query Match 34.8%; Score 40; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YQTKVNLL 8
| | | | | | | |
Db 15 YQTKVNLL 22

Search completed: December 4, 2002, 13:38:07
Job time : 15 secs

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